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(54) Title: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS

(57) Abstract: Recombinant adenovirus and methods of administration to a host are provided for eliciting immune response of the host to human immunodeficiency virus (HIV). The recombinant adenovirus is capable of expressing multiple wild type or mutant HIV antigens such as HIV envelope proteins without the cleavage site or the cytosolic domain, structural proteins such as Gag and its proteolytical fragments in a natural, secreted or membrane-bound form, HIV enzymes such as reverse transcriptase, protease and integrase, and regulatory proteins such as Tat, Rev and Nef. Immuno-stimulators such as cytokines can also be expressed by the recombinant adenovirus to further enhance the immunogenicity of the HIV antigens.

GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS

BACKGROUND OF THE INVENTION

Field of the Invention

This invention relates to vaccines for stimulating immune responses in human and other hosts, and, in particular, relates to recombinant viruses that express heterologous antigens of human immunodeficiency virus (HIV) in a host and elicit immune response to HIV infection.

Background of the Invention

Current techniques for developing vaccines are largely based on the concept of using denatured virus or purified viral proteins made from bacteria. These types of vaccines may be effective for only a limited number of infectious agents, and the protection rates are limited.

For viruses that contain membrane (envelope) glycoproteins (GPs), including the Ebola virus and the HIV virus, use of denatured virus or purified viral proteins often does not work satisfactorily. There may be several reasons for this. First, the GPs of these viruses are sensitive to the denaturing procedures so that the epitopes of the proteins are altered by the denaturing process. Second, the sugar moieties of the GPs are important antigenic determinants for neutralizing antibodies. In comparison, proteins made in bacteria are not properly glycosylated and can fold into somewhat different structures that can have antigenecities different from those of the natural viral proteins. Further, many vaccines that are based on attenuated or denatured virus provide a weak immune response to poorly immunogenic antigens. In addition, the vaccine preparations frequently offer only limited protection, not life-long immunity as desired.

Other vaccine approaches express antigens by plasmids directly injected into the body, the so-called naked DNA or DNA vaccine technology. These methods involve the deliberate introduction of a DNA plasmid carrying an antigen-coding gene by transfecting cells with the plasmid in vivo. The plasmid expresses the antigen that causes an immune response. The immune

response stimulated by DNA vaccine can be very inefficient, presumably due to low levels of uptake of the plasmid and low levels of antigen expression in the cells. DNA vaccines are also characterized by an extremely short antigen expression period due to vector degradation. In addition, DNA vaccines are difficult and costly to produce in large amounts.

Replication-competent, live vaccinia viruses have also been modified for expression of the genes for hepatitis B (HBV), human immunodeficiency virus (HIV), influenza and malaria antigens. In some instances, though, the immune response of recombinant vaccines is often of limited nature and magnitude. Thus, for example, while peripheral immunization with vaccinia influenza recombinants provides good protection against lower respiratory tract infections, it fails to induce immunity in the upper respiratory tract. On the other hand, peripheral immunization with recombinant vaccines may prove ineffective when local rather than systemic immunity is required, as in, for example, the gastro-intestinal tract.

Vaccination with recombinant vaccinia virus expressing Ebola virus GP has been attempted to confer partial protection in guinea pigs. Gilligan, K.J., et al., *Vaccines*, 97:87-92 (1997). Vaccination with DNA constructs expressing either GP or nucleocapsid protein (NP) protects mice from lethal challenge with Ebola virus. Vanderzanden, L., et al., *Virology*, 246(1):134-44 (1998). However, each of these approaches has its own set of limitations that make them less then ideal choices for Ebola virus vaccines in humans. For example, vaccinia virus rapidly kills vector-infected cells. Consequently, the vaccine antigen is expressed for only a short time. However, the major limitation for this type of approaches is that the replication of vaccina virus causes the immune system to react mainly to the vaccinia proteins, only small portion of the immune responses is targeted to the antigen of the pathogenic virus. This phenomenon has been termed "antigen dilution".

Previous attempts to remedy these deficiencies, including expression of vaccine antigens through viruses having stronger promoters, such as poxvirus, have not met with significant success.

As yet, no vaccine has been effective in conferring protection against HIV infection. Attempts to develop vaccines have thus far failed. Certain antibodies reactive with HIV, notably anti-GP160/120 are present at high levels throughout both the asymptomatic and symptomatic phases of the HIV infection, suggesting that rather than playing a protective role, such antibodies

may in fact promote the attachment and penetration of the virus into the host cell. More significantly, current vaccines do not induce efficient cellular responses against the infected cells, the source of newly released virions.

SUMMARY OF THE INVENTION

Genetic viral vaccines are provided. These vaccines are designed to mimic natural infection of pathogenic viruses without causing diseases that are naturally associated with the pathogenic viruses in a host to be immunized, such as human, domestic animals and other mammals.

The vaccines are recombinant benign viruses that are replication deficient or incompetent. The benign viruses may be designed to express antigens from a wide variety of pathogens such as viruses, bacteria and parasites, and thus may be used to treat this wide variety of viruses, bacteria, and parasites that natively express these antigens. Infection of the benign virus causes host cells to express the antigens of the pathogenic virus and presents the antigen in its natural conformation and pathway as if the cell were infected by the pathogenic virus, and induces a strong and long-lasting immune response in the host.

In one embodiment, a recombinant benign virus is provided for eliciting an immune response in a host infected by the virus. The recombinant virus comprises: an antigen sequence heterologous to the benign virus that encodes a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the pathogenic virus and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus; and an immuno-stimulator sequence heterologous to the benign virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen. The recombinant virus is replication-incompetent and does not cause disease that is associated with the pathogenic virus in the host

In a variation of the this embodiment, the recombinant benign virus may be a replication-incompetent virus such as adenovirus, adeno-associated virus, SV40 virus, retrovirus, herpes simplex virus or vaccinia virus. Preferably, the benign virus does not have the pathologic regions of the native progenitor of the benign virus but retains its infectivity.

In a preferred embodiment, the benign virus is a replication-incompetent adenovirus, more preferably adenovirus type 5. The heterologous antigen sequence may be positioned in the E1, E3 or E4 region of the adenovirus. The immuno-stimulator sequence may be positioned in the E4, E3 or E1 region of the adenovirus.

In a variation of the preferred embodiment, the heterologous antigen sequence and the immuno-stimulator sequence are positioned in the E1, E3 or E4 region of the adenovirus, where the heterologous antigen sequence and the immuno-stimulator sequence are expressed from a promoter bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

Expression of the viral antigen or the immuno-stimulator may be controlled by a promoter homologous to the native progenitor of the recombinant virus. Alternatively, expression of the viral antigen may be controlled by a promoter heterologous to the native progenitor of the recombinant virus. For example, the promoter heterologous to the native progenitor of the recombinant virus may be a eukaryotic promoter such as insulin promoter, human cytomegalovirus (CMV) promoter and its early promoter, simian virus SV40 promoter, Rous sarcoma virus LTR promoter/enhancer, the chicken cytoplasmic β-actin promoter, and inducible promoters such as the tetracycline-inducible promoter.

The pathogenic virus may be any pathogenic virus that causes pathogenic effects or disease in human or other animals. Thus, the recombinant benign virus can be used as a vaccine for protecting the host from infection of the pathogenic virus.

In a variation, the pathogenic virus may be various strains of human immunodeficiency virus (HIV), such as HIV-1 and HIV-2. The viral antigen may be an HIV glycoprotein (or surface antigen) such as HIV GP120 and GP41, or a capsid protein (or structural protein) such as HIV P24 protein.

In another variation, the pathogenic virus may be Ebola virus. The viral antigen may be an Ebola glycoprotein or surface antigen such as Ebola GP1 or GP2 protein.

In yet another variation, the pathogenic virus may be hepatitis virus such as hepatitis A, B, C, D or E virus. For example, the viral antigen may be a surface antigen or core protein of hepatitis B virus such as the small hepatitis B surface antigen (SHBsAg) (also referred to as the Australia antigen), the middle hepatitis B surface antigen (MHBsAg) and the large hepatitis B surface antigen (LHBsAg). The viral antigen may be a surface antigen or core protein of hepatitis C virus such as NS3, NS4 and NS5 antigens.

In yet another variation, the pathogenic virus may be a respiratory syncytial virus (RSV). For example, the RSV viral antigen may be the

glycoprotein (G-protein) or the fusion protein (F-protein) of RSV, for which the sequences are available from GenBank.

In yet another variation, the pathogenic virus may be a herpes simplex virus (HSV) such as HSV-1 and HSV-2. For example, the HSV viral antigen may be the glycoprotein D from HSV-2.

In yet another variation, the viral antigen may be a tumor antigen, such as Her 2 of breast cancer cells and CD20 on lymphoma cells, a viral oncogene such as E6 and E7 of human papilloma virus, or a cellular oncogene such as mutated ras.

It is noted that, other virus-associated proteins or antigens are readily available to those of skill in the art. Selection of the pathogenic virus and the viral antigen associated with the pathogenic virus is not a limiting factor in this invention.

The recombinant virus also expresses an immuno-stimulator to mimic cytokine-releasing response of a host cell upon viral infection and further augments the immune response to the viral antigen co-expressed from the recombinant virus. The immuno-stimulator may preferably be a cytokine. Examples of cytokine include, but are not limited to, interleukin-2, interleukin-8, interleukin-12, β- interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor (G-CSF), and granulocyte-macrophage colony stimulating factor (GM-CSF).

The viral antigen may be a full-length antigenic viral protein or a portion of the antigenic viral protein that contains the predominant antigen, neutralizing antigen, or epitope of the pathogenic virus. Alternatively, the viral antigen contains the constant region of glycoproteins of at least two strains of the pathogenic virus.

In a variation, the viral antigen may be a modified antigen that is mutated from a glycoprotein of the pathogenic virus such that the viral antigen is rendered non-functional as a viral component but retains its antigenicity. Such modification of the viral antigen includes deletions in the proteolytic cleavage site of the glycoprotein, and duplications and rearrangement of immunosuppressive peptide regions of the glycoprotein.

In another embodiment, a recombinant adenovirus is provided for eliciting an immune response in a host infected by the virus. The recombinant virus comprises: an antigen sequence heterologous to adenovirus and encoding a viral antigen from a pathogenic virus, expression of the viral

antigen eliciting an immune response directed against the viral antigen upon infection of the host by the recombinant adenovirus.

In a preferred variation of the embodiment, the recombinant virus is a replication-incompetent adenovirus. In particular, the pathogenic virus is HIV, including various types (e.g., HIV-1 and HIV-2), strains (e.g, strain BH10 and pNL4-3 of HIV-1), isolates, clades within a group of isolates (e.g., clade A, B, C, D, E, F, and G of group M of HIV-1 isolates) of HIV. The viral antigen may be a 1) HIV glycoprotein (or surface antigen) such as HIV envelope protein Env, either full length wild type (gp160), truncated (e.g, gp120 and gp41), or modified with insertions, deletions or substitutions; 2) HIV structural protein Gag, either full length wild type, modified, or protease-processed products or fragments in various forms (e.g., natural, secreted, or membrane bound forms of HIV capsid proteins such as HIV p24 and p17; and 3) HIV regulatory proteins such as Tat, Vif, Nef, and Rev.

According to this variation, the HIV antigen is an HIV envelop protein encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 14, 16, 20, 21, 22, 23, and 24. The polynucleotide may further encode HIV regulatory proteins such as Tat, Vif, Nef, and Rev.

Also according to the variation, the HIV antigen is a modified HIV envelope protein that includes multiclade variable loops. Preferably, the multiclade variable loops are V3 loops from various clades such as clade A, B, C, D, E, F, and G of group M of HIV-1 isolates. The modified HIV envelope protein that includes multiclade variable loops may include two or more V3 loops from different HIV clades, preferably V3 loops encoded by polynucleotides selected from the group consisting of SEQ ID NOs: 25, 26, 27, 28, 29, 30, and 31. More preferably, the modified HIV envelope protein that includes multiclade variable loops is encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 32, 52, and 54.

Also according to the variation, the HIV antigen is an HIV structural protein. The HIV structural protein may be a full length wild type Gag encoded by SEQ ID NO: 17, or a proteolytic fragment of Gag such as p17/24, p17 and p24. The fragment p17/24 may be in natural form and encoded by SEQ ID NO: 34, in secreted form and encoded by SEQ ID NO: 34, or in membrane bound form and encoded by SEQ ID NO: 36. The fragment p17 may be in natural form and encoded by SEQ ID NO: 40, in secreted form and encoded by SEQ ID NO: 41, or in membrane bound form and encoded by SEQ ID NO: 42.

Similarly, p24 may be in natural form and encoded by SEQ ID NO: 46, in secreted form and encoded by SEQ ID NO: 47, or in membrane bound form and encoded by SEQ ID NO: 48.

The recombinant virus may further comprise a polynucleotide encoding an HIV protease PI such as SEQ ID NO: 56, expression of which facilitates proteolytic processing of Gag expressed from the same recombinant virus or from another vector. PI may be expressed as a fusion protein with Gag, or separately from a different promoter or from the same promoter for Gag via an IRES or splicing donor/acceptor mechanism.

The recombinant virus may further comprise a polynucleotide encoding a fusion protein of HIV protease PI and HIV reverse transcriptase RT, PI-RT. PI may be expressed as a fusion protein with Gag, or separately from a different promoter or from the same promoter for Gag via an IRES or splicing donor/acceptor mechanism.

The recombinant virus may further comprise a polynucleotide which is an HIV *Pol* gene and encodes the HIV enzyme proteins: HIV protease PI, reverse transcriptase RT, and integrase IN. Pol may be expressed as a fusion protein with Gag, or separately from a different promoter or from the same promoter for Gag via an IRES or splicing donor/acceptor mechanism.

Optionally, the recombinant virus may further comprise an immuno-stimulator sequence heterologous to the recombinant virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen.

The present invention also provides viral vaccines that present multiple antigens to the host to further mimic natural infection of a native pathogenic virus and induce strong and long-lasting immune response to various strains or types of the pathogenic virus in the host.

In one embodiment, a recombinant virus is provided as a viral vaccine for eliciting an immune response in a host infected by the virus. The recombinant virus comprises: a plurality of antigen sequences heterologous to the recombinant virus, each encoding a viral antigen from a same pathogenic virus, different strains of a pathogenic virus, or different kinds of pathogenic viruses, expression of the plurality of the antigen sequences eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus.

The recombinant virus may preferably be replication-incompetent and not cause malignancy in the host naturally associated with pathogenic virus.

According to the embodiment, the recombinant virus may be any virus, preferably replication-incompetent adenovirus, adeno-associated virus, SV40 virus, retrovirus, herpes simplex virus or vaccinia virus. The benign virus may also preferably have the pathologic regions of the native progenitor of the benign virus deleted but retain its infectivity.

Also according to the embodiment, the plurality of the antigen sequences may be multiple copies of the same antigen sequence or multiple antigen sequences that differ from each another.

In a variation of the embodiment, at least two of the plurality of the antigen sequences are expressed from a promoter bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

Optionally, at least two of the plurality of the antigen sequences are expressed from a promoter to produce a fusion protein.

Also according to the embodiment, the viral genome further comprises at least one promoter heterologous to the native progenitor of the recombinant virus that controls the expression of at least two of the plurality of the antigen sequences. Examples of the promoter heterologous to the native progenitor of the recombinant virus include, but are not limited to, insulin promoter, CMV promoter and its early promoter, SV40 promoter, retrovirus LTR promoter/enhancer, the chicken cytoplasmic β-actin promoter, and inducible promoters such as tetracycline-inducible promoter.

Also according to the embodiment, the plurality of antigen sequences may be a combination of antigens from at least two strains of the pathogenic virus.

Optionally, the plurality of antigen sequences may be a combination of antigens from at least two different pathogenic viruses. For example, the plurality of antigen sequences may be a combination of antigens from HIV-1, HIV-2, herpes simplex virus type 1, herpes simplex virus type 2, Ebola virus, Marburg virus, Arbovirus (a group of viruses carried by mosquitoes that cause encephalitis, yellow fever, and dengue), and hepatitis A, B, C, D, and E viruses.

In a variation of the embodiment, the recombinant virus may further comprise one or more immuno-stimulator sequences that are heterologous to the benign virus and encodes an immuno-stimulator whose expression in the

host enhances the immunogenicity of the viral antigen. For example, the immuno-stimulator may be a cytokine. Examples of the cytokine include, but are not limited to, interleukin-2, interleukin-4, interleukin-12, β- interferon, λ-interferon, γ-interferon, G-CSF, and GM-CSF.

According to the variation, the one or more immuno-stimulator sequences may be multiple copies of the same immuno-stimulator sequence or multiple immuno-stimulator sequences that differ from each other.

Optionally, at least two of the immuno-stimulator sequences may be expressed from a promoter multicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism. Alternatively, at least two of the immuno-stimulator sequences may be expressed from a promoter to form a fusion protein.

The present invention also provides genetic vaccines that elicit strong and long-lasting immune response to pathogenic bacteria. In one embodiment, a recombinant virus is provided as a genetic bacteria vaccine for eliciting an immune response in a host infected by the recombinant virus. The recombinant virus comprises: a plurality of antigen sequences heterologous to the recombinant virus, each encoding a bacterial antigen from a pathogenic bacteria, expression of the plurality of the bacterial antigen sequences eliciting an immune response directed against the bacterial antigen and cells expressing the bacterial antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not cause malignancy naturally associated with the pathogenic bacteria in the host.

The pathogenic bacteria may be any pathogenic bacteria that causes pathogenic effects or diseases in a host, such as *bacillus tuberculoses*, *bacillus anthracis* (causing vegetative anthrax), and *spirochete Borrelia burgdorferi* that causes the Lyme disease in animals. The plurality of antigen sequences may encode lethal factors, protective antigen, edema factors of the pathogenic bacteria, or combinations thereof.

The present invention also provides vaccines against parasites that elicit strong and long-lasting immune response to pathogenic parasites. In one embodiment, a recombinant virus is provided as a parasite vaccine for eliciting an immune response in a host infected by the recombinant virus. The recombinant virus comprises: a plurality of antigen sequences heterologous to the benign virus, each encoding a parasitic antigen from a pathogenic parasite,

expression of the plurality of the parasitic antigen sequences eliciting an immune response directed against the parasitic antigen and cells expressing the parasitic antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not cause a malignancy naturally associated with the pathogenic parasite in the host.

The pathogenic parasite may be any pathogenic parasites that cause pathogenic effects or diseases in a host, such as malaria and protozoa such as Cryptosporidium, Eimeria, Histomonas, Leucocytozoon, Plasmodium, Toxoplasma, Trichomonas, Leishmania, Trypanosoma, Giardia, Babesia, and Theileria. The plurality of antigen sequences may encode coat proteins, attachment proteins of the pathogenic parasites, or combinations thereof.

The present invention also provides pharmaceutical compositions that include the viral vaccines of the present invention. The pharmaceutical composition may include any of the recombinant viruses described above and a pharmaceutically acceptable carrier or diluent.

The pharmaceutical composition may also include an adjuvant for augmenting the immune response to the viral antigen expressed from the recombinant virus. Examples of the adjuvant include, but are not limited to, bacillus Calmette-Guerin, endotoxin lipopolysaccharide, keyhole limpet hemocyanin, interleukin-2, GM-CSF, and cytoxan.

The present invention also relates to kits. These kits may include any one or more vaccines according to the present invention in combination with a composition for delivering the vaccine to a host and/or a device, such as a syringe, for delivering the vaccine to a host.

The present invention also provides methods for enhancing the immunity of a host with the recombinant viruses described above.

In one embodiment, the method comprises: administering to the host a recombinant virus in an amount effective to induce an immune response. The in the recombinant virus comprises: an antigen sequence heterologous to the recombinant virus that encodes a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus; and an immuno-stimulator sequence heterologous to the benign virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral

antigen. The recombinant virus may preferably be replication-incompetent and not cause malignancy naturally associated with the pathogenic virus in the host.

The recombinant virus may be administered to the host via any pharmaceutically acceptable route of administration. The recombinant virus may be administered to the host via a route of intramuscular, intratracheal, subcutaneous, intranasal, intradermal, intramucosally, rectal, oral and parental administration.

In another embodiment, a method is provided for enhancing the immunity of a host to a pathogenic virus with multiple antigens. The method comprises: administering to the host a recombinant virus in an amount effective to induce an immune response. The recombinant virus comprises: a plurality of antigen sequences heterologousto the benign virus, each encoding a viral antigen from a pathogenic virus, expression of the plurality of the antigen sequences eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not cause malignancy naturally associated with the pathogenic virus in the host.

Optionally, the recombinant virus may further comprise one or more immuno-stimulator sequences heterologous to the recombinant virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen.

In yet another embodiment, a method is provided for enhancing the immunity of a host to a pathogenic virus by using multiple recombinant viral vaccines (or viruses). Multiple recombinant viruses may carry different antigens in each recombinant virus. The multiple recombinant viruses may be administered simultaneously or step-wise to the host.

The method comprises: administering to a host a first and second recombinant viruses in an amount effective to induce an immune response. The first recombinant virus comprises: an antigen sequence heterologous to the first recombinant virus that encodes a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus. The second recombinant virus comprises: an immuno-stimulator sequence heterologous to the recombinant

virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen. The first and second recombinant viruses may preferably be replication-incompetent and not cause a malignancy naturally associated with the pathogenic virus in the host.

According to the embodiment, the first and second recombinant virus may be any benign virus, such as replication-incompetent adenovirus, adeno-associated virus (AAV), SV40 virus, retrovirus, herpes simplex virus, Alpha virus, Venezuelan Equine Encephalitis (VEE) virus and vaccinia virus.

Optionally, both the first and second recombinant viruses may be replication-incompetent adenovirus. Also optionally, one of the first and second recombinant viruses may be recombinant adenovirus and the other may be recombinant AAV, SV40 virus, retrovirus, herpes simplex virus, Alpha virus, Venezuelan Equine Encephalitis (VEE) virus or vaccinia virus.

In yet another embodiment, a method is provided for enhancing the immunity of a host to a pathogen. The method comprises: administering to the host a recombinant virus and one or more immuno-stimulators. The recombinant virus may be any of the recombinant viruses described above. In particular, the recombinant virus comprises one or more antigen sequences heterologous to the recombinant virus that encode one or more antigens from the pathogen. Expression of the antigen elicits an immune response directed against the antigen and cells expressing the antigen in the host upon infection of the host by the recombinant virus. The recombinant virus is preferably replication-incompetent and does not cause a malignancy naturally associated with the pathogen in the host. The pathogen may be a pathogenic virus such as HIV, hepatitis virus and Ebola virus, a pathogenic bacteria or parasite.

According to this embodiment, the immuno-stimulator may be any molecule that enhances the immunogenicity of the antigen expressed by the cell infected by the recombinant virus. Preferably, the immuno-stimulator is a cytokine, including, but not limited to Interleukin-2, interleukin-8, interleukin-12, β-interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor, granulocyte-macrophage colony stimulating factor, and combinations thereof. The cytokine may be administered into the host in a form of purified protein alone or formulated with one or more pharmaceutically acceptable excipients. Alternatively, the cytokine may be administered in a form of expression vector that expresses the coding sequence of the cytokine upon transfecting or transducing the cells of the host.

According to any of the above embodiments of the methods, the method may further comprise: administering to the host the recombinant virus again to boost the immune response. Such a booster inoculation with the recombinant virus is preferably conducted several weeks to several months after the primary inoculation. To insure sustained high levels of protection against infection or an efficacious treatment of the disease(s) caused by infection of the pathogen, it may be helpful to re-administer the booster immunization to the host at regular intervals, for example, once every several years. The recombinant virus administered in the booster immunization may be the same as or different from the recombinant virus administered in the primary immunization.

Also according to any of the above embodiments of the methods, the method may further comprise: administering to the host a plasmid vector that encodes the same or different antigen(s) as that (or those) encoded by the recombinant virus. The plasmid vector is preferably a eukaryotic plasmid expression vector that expresses the antigen(s) upon transfection of the cells in the host.

Also according to any of the above embodiments of the methods, the method may further comprise: administering to the host a second recombinant virus to boost the immune response and/or to minimize neutralizing effects of the host's immune system on the recombinant viruses.

Optionally, the second recombinant virus comprises a second antigen sequence from a second pathgen that is different from the first antigen sequence comprised in the first recombinant virus administered in the primary immunization. Preferably, the second antigen sequence encodes the same type of antigen as that encoded by the first antigen sequence but from a different strain, serotype, or subtype/clade of the same pathogen. Alternatively, the second antigen may be a different type of antigen compared to the first antigen, for example, the first antigen being a surface protein and second antigen being a core protein of the same or different pathogen.

Also according to any of the above embodiments of the methods, the method may further comprise: administering to the host a viral vector prior to, concurrently, or post the administration of any of the above embodiment of the recombinant virus to minimize neutralizing effects of the host's immune system on the recombinant virus. Preferably, the viral vector is administered post the administration of the recombinant virus.

The viral vector may be the native progeny of the recombinant virus. For example, the viral vector may be the wildtype adenovirus type 5 (Ad5) whereas the recombinant virus is a genetically modified Ad5.

Optionally, the viral vector may be the wildtype of or a genetically modified virus that is a different serotype of the recombinant virus. For example, the recombinant virus may be a genetically modified Ad5 whereas the viral vector is the wildtype of or a genetically modified adenoviral vector serotype other than Ad5, for example, serotype 1-4 or 6-51. It is noted that other serotypes discovered and/or classified later also fall within the scope of the invention.

Also optionally, the viral vector may be a different virus from the recombinant virus. For example, the recombinant virus may be a genetically modified Ad5 whereas the viral vector is a genetically modified AAV, SV40 virus, retrovirus, herpes simplex virus, Alpha virus, Venezuelan Equine Encephalitis (VEE) virus or vaccinia virus. The viral vector may or may not comprise a heterologou antigen sequence. Preferably, the viral vector may comprise another antigen sequence which is the same or different from the antigen sequence carried by the recombinant virus.

Also optionally, the viral vector may be a chimeric vector modified based on the native progenitor of the recombinant virus. For example, if the native progenitor of the recombinant virus is adenovirus type 5, the viral vector may be a chimeric adenovirus type 5 with certain regions of the backbone changed from type 5 to the corresponding regions from other adenovirus serotypes. For example, the fiber knob, shaft, and/or penton base in the backbone of adenovirus type 5 can be replaced by the corresponding region(s) of the backbone from adenovirus serotype 1-4, and 6-51.

Also optionally, the viral vector also comprises one or more heterologous antigen sequence and/or immuno-stimulator sequence which are the same or different from those in the recombinant virus.

The methods described above may be used for prevention or treatment of diseases. In the method of treatment, the administration of the recombinant viruses of the present invention may be for either "prophylactic" or "therapeutic" purpose. When provided prophylactically, the recombinant virus is provided in advance of any symptom. The prophylactic administration of the recombinant virus serves to prevent or ameliorate any subsequent infection or disease. When provided therapeutically, the recombinant virus is provided at (or after)

the onset of a symptom of infection or disease. Thus, the present invention may be provided either prior to the anticipated exposure to a disease-causing agent or after the initiation and/or progression of the infection or disease.

It is noted that the innovative approaches of the present invention may also be employed in construction of cancer vaccines. For example, sequences encoding tumor-specific antigens may substitute the antigen sequence encoding viral antigen in any of the above embodiments of the recombinant virus and methods of using the same. Expression of tumor-specific antigens in the host should elicit specific immune response for prevention in patients with an increased risk of cancer development (i.e., preventive immunization) or to enhance the treatment of cancer with other therapeutics, prevention of disease recurrence after primary surgery (anti-metastatic vaccination), or as a tool to expand the number of CTL in vivo, thus improving their effectiveness in eradication of diffuse tumors (treatment of established disease). In addition, the methods of the present invention may elicit an immune response in a patient that is enhanced ex vivo prior to being transferred back to the tumor bearer (i.e., the adoptive immunotherapy).

Also according to any of the above embodiments of the methods, the method may further comprise: harvesting serum from the host after the administration of the recombinant virus. The harvested serum should contain antibodies against the antigen(s) encoded by the recombinant virus. Optionally, the method may further comprise: isolating antibody or antibodies against the pathogen from the host after the administration of the recombinant virus. The harvested serum or isolated antibody can be stored for certain periods of time for further uses. For example, a healthy human volunteer can serve as the host and the serum or antibody collected from him/her may be administered back to him/herself or a different person later to in anticipation or in the event of infection of the pathogen as prophylactic or therapeutic agent by eliciting passive immunity against the pathogen. Optionally, the host may be a non-human animal and the serum harvested or antibody isolated from the animal immunized by the recombinant virus may be used as a prophylactic or therapeutic agent to treat a human or non-human animal in anticipation or in the event of infection of the pathogen such as in the outbreak of biological warfare.

It should be noted that modifications and changes can be made in the DNA sequence of any of the above-described antigens and immuno-

stimulators included in the recombinant virus and still maintain functional equivalence of the mutant. For example, wildtype codons for the above-described antigens can be replaced with codons that are preferred by the host to be immunized, e.g., a human. The resulting mutants fall within the scope of the present invention.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A-1C illustrate an example of how to construct a genetic vaccine of the present invention.

Figure 1A illustrates an example of a shuttle vector pLAd.Antigen carrying multiple antigen genes such as Antigen 1 and Antigen 2 which can be expressed from a CMV_{ie} promoter bicistronically via a splicing donor-acceptor mechanism at the SD and SA sites.

Figure 1B illustrates an example of a shuttle vector pRAd.Cytokines carrying multiple cytokine genes such as IL-2, INF, and IL-8 genes which can be expressed from a CMV_{ie} promoter bicistronically via an internal ribosomal entry site IRES and a splicing donor-acceptor mechanism at the SD and SA sites.

Figure 1C illustrates an example of constructing a genetic vaccine by ligating with an adenoviral backbon with a fragment that is derived from the shuttle vector pLAd.Antigen and contains multiple antigen genes and a fragment that is derived from the shuttle vector pRAd.Cytokines and contains multiple cytokine genes.

Figure 2 illustrates the wild-type GP gene, which encodes the two forms of glycoproteins (sGP and GP), contains a RNA editing signal that results in un-edited and edited mRNAs. The sGP is synthesized from an un-edited mRNA and the GP is synthesized from an edited mRNA (having an insertion in one of the seven uridines). **Figure 2** also depicts the modifications made to the RNA to prevent the synthesis of sGP. The RNA editing site is modified from UUU UUU U to UUC UUC UU. This modification removes the editing signal and results in the mRNA coding only for the GP.

Figure 3 illustrates the modification of the immunosuppressive peptide (IS) located in GP2. **Figure 3A** shows the wild type GP. **Figure 3B** shows GP with the 10 amino acid deletion of the IS peptide. **Figure 3C** shows the IS

peptide, which is split, reversed and duplicated. Abbreviations: FP, Fusion peptide; IS, Immunosuppressive peptide; TM, Transmembrane domain.

Figures 4A and **4B** illustrate a procedure used to create a recombinant adenoviral vector as a genetic vaccine against Ebola virus.

Figures 4A illustrates a shuttle vector pLAd/EBO-GP carrying the GP gene of Ebola virus an antigen, and a shuttle vector pRAdIL2,4 carrying the IL-2 and IL-4 gene.

Figure 4B illustrates the construction of a recombinant adenoviral vector by ligating an adenoviral backbone with a fragment that is derived from the shuttle vector pLAd/EBO-GP and contains the GP gene and a fragment that is derived from the shuttle vector pRAdIL2,4 and contains IL-2 and IL-4 genes.

Figure 5 illustrates a complex adenoviral vector as an example of the genetic vaccine of the present invention. The Ebola viral GP gene is expressed by a CMVie promoter in the E1 region. The GP gene is followed by INF-γ and GM-CSF which are expressed by two IRES sequences. This configuration allows for the expression of three proteins from a single mRNA. Expression of IL-2 and IL-4 is controlled by a second CMVie promoter as a bi-cistronic cassette, and followed by a second bi-cistronic cassette that expressed the two subunits of IL12 in the E4 region by a SV40 early promoter.

Figure 6 shows relative titers of antibody against HIV antigens in a group of mice.

Figure 7 shows relative titers of antibody against HIV antigens in another group of mice.

Figure 8A-C show INF-γ secretion from activated splenocytes harvested from mice inoculated with adenoviral vectors in response to target cell stimulation.

Figure 9 shows granzyme A secretion from activated splenocytes harvested from mice inoculated with adenoviral vectors in response to target cell stimulation.

Figure 10A shows relative titers of antibody against HBV surface antigen in a group of mice.

Figure 10B shows relative titers of antibody against HBV surface antigen in another group of mice.

Figure 11A shows relative titers of antibody against HBV core antigen in a group of mice.

Figure 11B shows relative titers of antibody against HBV core antigen in another group of mice.

Figure 12A shows relative titers of antibody against HIV Gag in mice in week 10 post-immunization with Ad-3C/$E^{m}\Delta C\Delta T^{300}$-G.

Figure 12B shows relative titers of antibody against HIV Gag in mice in week 14 post-immunization/week 3 post-boost with Ad-3C/$E^{m}\Delta C\Delta T^{300}$-G.

Figure 13A shows relative titers of antibody against HIV Gag in mice in week 10 post-immunization with Ad-3C/$E^{m}\Delta C\Delta T^{99}$-G.

Figure 13B shows relative titers of antibody against HIV Gag in mice in week 14 post-immunization/week 3 post-boost with Ad-3C/$E^{m}\Delta C\Delta T^{99}$-G.

Figure 14A shows results of the granzyme A assays for serie 1 mice at week 4, 6, 8 post-immunization and week 12/1, 13/2, 14/3 (prime/boost) post-secondary inoculation with Ad.3C.env.gag.

Figure 14B shows the results of the granzyme A assays for serie 2 mice at week 2, 4, 6, 8 post-immunization with Ad.3C.env.gag.

Figure 15A shows the ELISPOT results for the four mice in serie 1 at week 13/2 post-prime/boost with Ad.3C.env.gag.

Figure 15B shows the ELISPOT results for the four mice in serie 1 at week 13/2 post-prime/boost with Ad.3C.env.rev.gag.

Figure 16A illustrates a shuttle vector pLAd-E.T.R.

Figure 16B illustrates a shuttle vector pRAd-ORF6-IL2.

Figure 17A illustrates a shuttle vector pRAd-ORF6-cmv- $E^{m}\Delta C\Delta T^{300}$-G.

Figure 17B illustrates a shuttle vector pLAd-3C.

Figure 18 illustrates a shuttle vector pRAd-$E^{m}\Delta C\Delta T^{99}$.T.R-G

Figure 19A illustrates a shuttle vector pLAd- $E^{m}\Delta V_{1,2}\ \Delta C\ \Delta T$.T.R-IL2.

Figure 19B illustrates a shuttle vector pRAd-ORF6-G.IL2.

Figure 20 illustrates a shuttle vector pLAd-$E^{m}\Delta C$.T.R.N.

Figure 21 illustrates a shuttle vector pLAd-$E^{m}\Delta C$.N.

Figure 22 illustrates a shuttle vector pLAd-$E^{m}\Delta C\ \Delta T^{300}$.T.

Figure 23A illustrates a shuttle vector pLAd-$E^{m}\Delta C$.

Figure 23B illustrates a shuttle vector pRAd-ORF6-$E^{m}\Delta C$.

Figure 24 illustrates a process for constructing a multi-clade insert by PCR.

Figure 25 illustrates a shuttle vector pLAd-E^{m}.V3.

Figure 26 illustrates a shuttle vector pLAd-E^{m}.2xV3.

Figure 27A illustrates a shuttle vector pRAd-ORF6-p17/p24.

Figure 27B illustrates a shuttle vector pRAd-ORF6-p17/p24sec.

Figure 27C illustrates a shuttle vector pRAd-ORF6-p17/p24MB.

Figure 28A illustrates a shuttle vector pRAd-ORF6-p17.

Figure 28B illustrates a shuttle vector pRAd-ORF6-p17sec.

Figure 28C illustrates a shuttle vector pRAd-ORF6-p17MB.

Figure 29A illustrates a shuttle vector pRAd-ORF6-p24.

Figure 29B illustrates a shuttle vector pRAd-ORF6-p24sec.

Figure 29C illustrates a shuttle vector pRAd-ORF6-p24MB.

Figure 30A-B illustrate a process of construction of Ad-E^{m}.2xV3^{m}/p17/p24MB.

Figure 31A-B illustrate a process of construction of Ad-E^{m}.2xV3^{m}/p17MB.

Figure 32A-B illustrate a process of construction of Ad-E^{m}.2xV3^{m}/p24MB.

Figure 33 illustrates a shuttle vector pLAd-$E^{m}\Delta C\Delta T^{300}$.2xV3^{m}.T.

Figure 34 illustrates a shuttle vector pLAd-$E^{m}\Delta C\Delta T^{99}$.2xV3^{m}.T.R.

Figure 35 illustrates a shuttle vector pRAd-ORF6-G.PI.

Figure 36 illustrates a shuttle vector pRAd-ORF6-G-PI.

Figure 37 illustrates a cloning vector SD/SA1.2.3

Figure 38 shows DNA sequence encoding Env/Tat/Rev from HIV-1 strain BH10.

Figure 39 shows DNA sequence encoding a mutated IL-2 (IL-2ΔX).

Figure 40 shows DNA sequence encoding a modified Env ($E^{m}\Delta C\Delta T$ (BH10).

Figure 41A shows DNA sequence encoding the full length HIV Gag.

Figure 41B shows amino acid sequence of the full length HIV Gag.

Figure 42 shows DNA sequence encoding Env, and full length Tat and Rev.

Figure 43 shows DNA sequence encoding $E^{m}\Delta V_{1,2}\,\Delta C\,\Delta T.T.R.$

Figure 44 shows DNA sequence encoding $E^{m}\Delta C.T.R.N.$

Figure 45 shows DNA sequence encoding $E^{m}\Delta C.N.$

Figure 46 shows DNA sequence encoding $E^{m}\Delta C\Delta T^{300}.T.$

Figure 47 shows DNA sequence encoding $E^{m}/E^{m}.$

Figure 48 shows DNA sequences of V3 loops of clade B, A, C, D, E, F, and G.

Figure 49A shows DNA sequence encoding a modified Env including multi-clade V3 loops.

Figure 49B shows amino acid sequence encoding a modified Env including multi-clade V3 loops.

Figure 50A shows DNA sequence encoding p17/p24 in natural form, secreted form, and membrane bound form, respectively.

Figure 50B shows amino acid sequence of p17/p24 in natural form, secreted form, and membrane bound form, respectively.

Figure 51A shows DNA sequence encoding p17 in natural form, secreted form, and membrane bound form, respectively.

Figure 51B shows amino acid sequence of p17 in natural form, secreted form, and membrane bound form, respectively.

Figure 52A shows DNA sequence encoding p24 in natural form, secreted form, and membrane bound form, respectively.

Figure 52B shows amino acid sequence of p24 in natural form, secreted form, and membrane bound form, respectively.

Figure 53A shows DNA sequence encoding a modified Env including multi-clade V3 loops, and Tat.

Figure 53B shows amino acid sequence of a modified Env including multi-clade V3 loops, and Tat.

Figure 54A shows DNA sequence encoding a modified Env including multi-clade V3 loops, Tat, and Rev.

Figure 54B shows amino acid sequence of a modified Env including multi-clade V3 loops, Tat, and Rev.

Figure 55A shows DNA sequence encoding an HIV protease PI.

Figure 55B shows amino acid sequence of an HIV protease PI.

Figure 56A shows DNA sequence encoding HIV Gag-PI.

Figure 56B shows amino acid sequence of HIV Gag-PI.

Figure 57 shows PCR primers for cloning V3 loops from multiple HIV clades.

Figure 58 illustrates a shuttle vector pRAd-ORF6-Gag/Pl-RT.

Figure 59 illustrates a shuttle vector pRAd-ORF6-Gag-Pl-RT.

Figure 60 illustrates a shuttle vectorpRAd-ORF6-Gag/Pol.

Figure 61 illustrates a shuttle vectorpRAd-ORF6-Gag-Pol.

Figure 62 illustrates a right shuttle vector pR-Ad.5/35-6m.

Figure 63 shows various embodiments of chimeric vectors having the individual domains of the Ad5 fiber regions substituted with the corresponding domains of Ad35 fiber region.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides genetic vaccines, pharmaceutical compositions including the vaccines and methods of immunizing a host against infection of a wide range of pathogenic viruses, bacteria and parasites. The genetic vaccines are recombinant benign viruses that are replication deficient and do not cause malignancy in the host to be immunized. Vaccination using the genetic vaccines of the present invention mimics natural viral infection in that the antigen(s) expressed by the cell infected by the genetic vaccine is presented to the host immune system in its natural conformation and by a "inside-out" mechanism, as compared with the conventional "outside-in" approach of vaccination using denatured protein or virus as a vaccine. The recombinant virus is capable of expressing multiple pathogenic antigens, mimicking natural pathogen infection. In particular, multiple pathogenic antigens such as a combination of an HIV envelop protein Env and structural protein Gag, either wildtype or mutant, can be expressed by the recombinant virus to elicit not only humoral immune response (i.e., production of antibody from B cells, helper T cells, and suppressor T cells), but also cellular response by producing cytotoxic T lymphocytes (CTL) directed specifically to these antigens. Further, the pathogenic antigen that is naturally expressed as an intracellular protein can be modified to be secretable and rendered bound to the cell surface, thus better presenting the antigen to the body's immune system. In addition, the cell infected by the genetic vaccine may also release high levels of cytokine, thereby further mimicking the natural response of the cell under stress induced by viral infection and yet not causing pathogenic effects on the cells. Mistaken by such a "signal of pathogenic viral infection", the host immune system mounts a strong immune defense against the antigen presented by the infected cell. Therefore, in a sense, the genetic vaccine of the present invention behaves like a "sheep in wolf's clothing", presenting the viral antigen to induce a strong immune response and yet not causing the detrimental effects that the pathogens would cause on the host. The recombinant viruses of the present invention can not only be used as a vaccine to prevent infection of the pathogen but also as a therapeutic agent to treat diseases associated with the infection of the pathogen.

In one embodiment, a recombinant virus is provided for eliciting an immune response in a host infected by the virus. The recombinant virus comprises: an antigen sequence heterologous to the recombinant virus and encoding a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus; and an immuno-stimulator sequence heterologous to the recombinant virus and encoding an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen. The recombinant virus is replication-incompetent and does not cause the malignancy naturally associated with the pathogenic virus in the host.

In another embodiment, a recombinant virus is provided as a viral vaccine for eliciting an immune response against multiple antigens in a host infected by the virus. The recombinant virus comprises: a plurality of antigen sequences heterologous to the benign virus, each encoding a different viral antigen from one or more pathogenic viruses, expression of the plurality of the antigen sequences eliciting an immune response directed against the viral antigens and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not cause the malignancy that is naturally associated with the pathogenic virus(es) in the host.

The vaccines of the present invention can be used to immunize the host against a wide variety and different strains of pathogenic viruses such as HIV-1, HIV-2, herpes simplex virus type 1, herpessimplex virus type 2, Ebola virus, Ebola virus, and hepatitis A, B, C, D, and E viruses, or pathogenic bacteria such as *bacillus tumerculoses* and *bacillus anthracis*.

The recombinant vaccine of the present invention is a recombinant virus that contains nucleic acid sequences encoding one or more viral antigens in the viral genome. When a host is immunized by the recombinant vaccine, i.e., infected by the recombinant virus, the infection of the virus in a host cell results in expression of the viral antigen which is present on the surface of the infected cell. Since expression of the viral antigen is driven by a strong promoter, expession can be maintained at a high level. Upon recognizing the large amount viral antigen on the cell surface, the host immune system mounts a strong defense against the viral antigen, thereby

achieving long-lasting immunity against the pathogenic virus from which the viral antigen is derived.

Compared with immunization with vaccines that are isolated proteins expressed by bacteria, yeast or insect cells, the viral antigen expressed from the recombinant virus of the present invention better mimics the natural viral antigen in its structure and function. Isolated protein vaccine may not adopt the native conformation of the natural viral antigen and may not be properly glycosylated in the bacteria, yeast or insect cells. When such an isolated protein vaccine is injected into the host, this antigen is presented from the outside of the host cell. This conventional "outside-in" approach often does not generate strong, long-lasting immune response, presumably due to the altered antigenicity of the vaccine and quick clearance of the protein vaccine by the immune scavenging cells.

In contrast, the genetic vaccine of the present invention, i.e., the recombinant virus, presents the viral antigen by an "inside-out" mechanism. The viral antigen is expressed after infection of the recombinant virus in the host cells. This better mimics the natural production and presentation of the viral antigen by the pathogenic virus.

By using a replication incompetent virus that is incapable of spreading beyond initially infected cells, the present invention dramatically reduces the risk of side effects that may potentially be generated by using replication-competent, live virus. For example, vaccines based on live vaccinia virus can replicate in the host cells, which can impose a high level of stress on the host cell and eventually lead to cell death.

Moreover, compared to the approach of using attenuated or inactive virus as a vaccine, the process of making the genetic vaccine of the present invention is much safer. Vaccination of a large population of people or animals demand large amounts of vaccines. For virulent viruses such as Ebola virus and HIV, large-scale production of attenuated or inactive virus from the live virus can pose a great danger to the environment and people who handle the live virus.

The recombinant virus of the present invention can be used to express multiple antigen sequences simultaneously from the same viral vector. Thus, the recombinant virus may encode multiple antigens from the same strain of pathogenic virus, from different strains of the same pathogenic viruses, or

from different antigens from different kind of viruses, bacteria or parasites. This enables the vaccines of the present invention to be utilized to immunize against a broad-spectrum of viruses and other infectious agents. Since these multiple antigen sequences are rearranged in the recombinant viral genome, the risk of potential recombination of these viral sequences to generate a pathogenic virus is virtually eliminated.

The genetic vaccine of the present invention also preferably express large amount of immunuo-stimulator, such as cytokine. In a natural process of viral infection, virus-infected cells display viral antigens on their surface in the context of the MHC-I receptor, while viral particles are digested by the professional antigen-presenting cells which display antigens in association with MHC-II receptors. In response to viral infection, a full range of cytokines and interferons are produced, resulting in a strong humoral and cellular response to the viral antigens. At the same, large numbers of memory cells remain to defeat any new infection. In vaccinations using isolated protein vaccines, the protein is quickly cleared by the immune scavenging cells. During this process, only MHC-II antigen presentation occurs and the cytokine-releasing response is absent or greatly diminished. As a result, little cellular response is generated and few "memory" cells are produced.

In comparison, co-expression of viral antigen and cytokine from the recombinant virus of the present invention effectively mimics the natural response of the host cell to viral infection by presenting the antigen on the surface of the infected and producing large amount of immuno-modulating cytokines. With the high levels of cytokine expressed from the host cells infected by the genetic vaccine, the host immune system would be "tricked" to mount a strong response to vaccine, thereby resulting in a longer-lasting immunity.

Additionally, although vaccination with the genetic vaccine mimics the natural viral infection of a pathogenic virus, the vaccine itself is a benign virus that does not have the detrimental effects of the pathogenic virus. For example, infection of a pathogenic virus such as HIV, influenza virus and Ebola virus has profound immuno-suppressing effects on the host, presumably due to the immuno-suppressing functions of the glycoproteins of the virus. According to the present invention, the viral antigen sequence carried by the genetic vaccine is preferred to have its pathogenic or immuno-

suppressing regions deleted. In a sense, the genetic vaccine of the present invention behaves like a "sheep in wolf's clothing", presenting the viral antigen to induce strong immune response and yet not causing detrimental effects on the host.

1. **The Genetic Vaccines of the Present Invention**

The present invention is directed to vaccines that mimic the features of a native pathogenic virus, but without eliciting immuno-suppression and pathogenicity, thus causing the host to mount an effective defense, while not being in any actual danger of infection. The genetic vaccines are replication incompetent or defective viruses into which one or more DNA sequences encoding one or more viral antigens are inserted into the regions of the viral genome non-essential to its infectivity. The recombinant virus expresses the viral antigens and elicits a cell-mediated immune response *in vivo* directed against the antigens and cells expressing the antigens.

In one embodiment, a recombinant virus is provided for eliciting an immune response in a host infected by the virus. The recombinant virus comprises: an antigen sequence heterologous to the recombinant virus that encodes a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the viral antigen and cells expressing the viralantigen in the host upon infection of the host by the recombinant virus; and an immuno-stimulator sequence heterologous to the recombinant virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen. The recombinant virus is replication-incompetent and does not cause a malignancy naturally associated with the pathogenic virus in the host.

The recombinant virus may be constructed from any virus as long as the native progenitor is rendered replication incompetent. For example, replication-incompetent adenovirus, adeno-associated virus, SV40 virus, retrovirus, herpes simplex virus or vaccinia virus may be used to generate the recombinant virus by inserting the viral antigen into the region non-essential to the infectivity of the recombinant virus. Therefore, it is preferred that the recombinant virus does not have the pathologic regions of the native progenitor of the benign virus but retains its infectivity to the host.

In a preferred embodiment, the recombinant virus is a replication-incompetent adenovirus.

The recombinant adenovirus of the present invention can direct high levels of antigen expression that provide strong stimulation of the immune system. The antigen expressed by cells infected by adenovirus is processed and displayed in the infected cells in a way that mimics pathogen-infected cells. This phase is believed to be very important in inducing cellular immunity against infected cells, and is completely lacking when conventional vaccination approaches are used. Further, the recombinant adenovirus may infect dendritic cells which are very potent antigen-presenting cells. Further, the recombinant adenovirus may also carry genes encoding immuno-enhancing cytokines to further boost immunity. Moreover, the recombinant adenovirus may naturally infect airway and gut epithelial cells in humans, and therefore the vaccine may be delivered through nasal spray or oral ingestion. In addition, the recombinant adenovirus of the present invention should be safe because it is replication-incompetent.

The heterologous antigen sequence may be positioned in the E1, E3 or E4 region of the adenovirus. The immuno-stimulator sequence may be positioned in the E1, E3 or E4 region of the adenovirus.

In a variation of the preferred embodiment, the heterologous antigen sequence and the immuno-stimulator sequence are positioned in the E1, E3 or E4 region of the adenovirus, where the heterologous antigen sequence and the immuno-stimulator sequence are expressed from a promoter bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

The expression of the viral antigen or the immuno-stimulator may be controlled by a promoter homologous to the native progenitor of the recombinant virus. Alternatively, the expression of the viral antigen may be controlled by a promoter heterologous to the native progenitor of the recombinant virus. For example, the promoter heterologous to the native progenitor of the recombinant virus may be a eukaryotic promoter such as insulin promoter, human cytomegalovirus (CMV) promoter and its early promoter, simian virus SV40 promoter, Rous sarcoma virus LTR promoter/enhancer, the chicken cytoplasmic β-actin promoter, and inducible promoters such as the tetracycline-inducible promoter.

The pathogenic virus may be any pathogenic virus that causes pathogenic effects or disease in a host such as human, domestic animals or other mammals. Thus, the recombinant virus can be used as a vaccine for protecting the host from infection of the pathogenic virus.

In a variation, the pathogenic virus may be various strains of human immunodeficiency virus (HIV), such as HIV-1 and HIV-2. The viral antigen may be a HIV glycoprotein (or surface antigen) such as HIV GP120 and GP41, a capsid protein (or structural protein) such as HIV P24 protein, or other HIV regulatory proteins such as Tat, Vif and Rev proteins.

In another variation, the pathogenic virus may be influenza virus. The viral antigen may be an influenza glycoprotein such as influenza HA1, HA2 and NA.

In another variation, the pathogenic virus may be Ebola virus. The viral antigen may be an Ebola glycoprotein or surface antigen such as Ebola GP1 and GP2 protein.

In yet another variation, the pathogenic virus may be hepatitis virus such as hepatitis A, B, C, D or E virus. The viral antigen may be a surface antigen or core protein of hepatitis A, B, C, D or E virus. For example, the viral antigen may be a surface antigen or core protein of hepatitis B virus such as the small hepatitis B surface antigen (SHBsAg) (also referred to as the Australia antigen), the middle hepatitis B surface antigen (MHBsAg) and the large hepatitis B surface antigen (LHBsAg). The viral antigen may also be a surface antigen or core protein of hepatitis C virus such as NS3, NS4 and NS5 antigens.

In yet another variation, the pathogenic virus may be a respiratory syncytial virus (RSV). For example, the RSV viral antigen may be the glycoprotein (G-protein) or the fusion protein (F-protein) of RSV, for which the sequences are available from GenBank.

In yet another variation, the pathogenic virus may be a herpes simplex virus (HSV) such as HSV-1 and HSV-2. For example, the HSV viral antigen may be the glycoprotein D from HSV-2.

In yet another variation, the viral antigen may be a tumor antigen or viral oncogene such as E6 and E7 of human papilloma virus, or cellular oncogenes such as mutated ras or p53.

It is noted that, other virus-associated proteins or antigens are readily available to those of skill in the art. Selection of the pathogenic virus and the viral antigen is not a limiting factor in this invention.

The viral antigen may be a full-length antigenic viral protein or a portion of the antigenic viral protein that contains the predominant antigen, neutralizing antigen, or epitope of the pathogenic virus. Alternatively, the viral antigen contains the conserved region of glycoproteins between at least two strains of the same pathogenic virus.

In a variation, the viral antigen may be a modified antigen that is mutated from a glycoprotein of the pathogenic virus such that the viral antigen is rendered non-functional as a viral component but retains its antigenicity. Such modification of the viral antigen includes deletions in the proteolytic cleavage site of the glycoprotein, and duplications and rearrangement of immunosuppressive peptide regions of the glycoprotein.

The recombinant virus also expresses an immuno-stimulator to mimic cytokine-releasing response of a host cell upon viral infection and further augments immune response to the viral antigen co-expressed from the recombinant virus. The immuno-stimulator may preferably be a cytokine. Examples of cytokine include, but are not limited to, interleukin-2, interleukin-4, interleukin-12, β- interferon, λ-interferon, =γ-interferon, granulocyte colony stimulating factor (G-CSF), and granulocyte-macrophage colony stimulating factor (GM-CSF).

In another embodiment, a recombinant virus is provided for eliciting an immune response in a host infected by the virus. The recombinant virus comprises: an antigen sequence heterologous to the recombinant virus that encodes a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus.

According to this embodiment, the recombinant virus is preferably be replication-incompetent adeno-associated virus, SV40 virus, retrovirus, herpes simplex virus or vaccinia virus. The benign virus may preferably have the pathologic regions of the native progenitor of the benign virus deleted but retains its infectivity to the host.

Optionally, the recombinant virus includes an immuno-stimulator sequence heterologous to the recombinant virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen.

The present invention also provides genetic vaccines that elicit strong and long-lasting immune response to pathogenic bacteria. In one embodiment, a recombinant virus is provided as a genetic bacteria vaccine for eliciting an immune response in a host infected by the recombinant virus. The viral genome of the recombinant virus comprises: a plurality of antigen sequences heterologous to the recombinant virus, each encoding a bacterial antigen from a pathogenic bacteria, expression of the plurality of the bacterial antigen sequences eliciting an immune response directed against the bacterial antigen and cells expressing the bacterial antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not cause a malignancy naturally associated with the pathogenic bacteria in the host.

The pathogenic bacteria may be any pathogenic bacteria that causes pathogenic effects or diseases in a host, such as *bacillus tuberculoses*, *bacillus anthracis*, and *spirochete Borrelia burgdorferi* that causes the Lyme disease in animals. The plurality of antigen sequences may encode lethal factors, protective antigen, edema factors of the pathogenic bacteria, or combination thereof.

The present invention also provides parasites vaccines that elicit strong and long-lasting immune response to pathogenic parasites. In one embodiment, a recombinant virus is provided as a parasite vaccine for eliciting an immune response in a host infected by the benign virus. The recombinant virus comprises: a plurality of antigen sequences heterologous to the recombinant virus, each encoding a parasitic antigen from a pathogenic parasite, expression of the plurality of the parasitic antigen sequences eliciting an immune response directed against the parasitic antigen and cells expressing the parasitic antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not a cause malignancy naturally associated with the pathogenic parasite in the host.

The pathogenic parasite may be any pathogenic parasite that causes pathogenic effects or diseases in a host, such as malaria and protozoa such as Cryptosporidium, Eimeria, Histomonas, Leucocytozoon, Plasmodium, Toxoplasma, Trichomonas, Leishmania, Trypanosoma, Giardia, Babesia, and Theileria. The plurality of antigen sequences may encode coat proteins, attachment proteins of the pathogenic parasites, or combinations thereof.

The present invention also provides viral vaccines that present multiple antigens to the host to further mimic natural infection of a native pathogenic virus and induce strong and long-lasting immune response to various strains or types of the pathogenic virus in the host.

In one embodiment, a recombinant virus is provided as a viral vaccine for eliciting an immune response in a host infected by the virus. The recombinant virus comprises: a plurality of antigen sequences heterologous to the recombinant virus, each encoding a viral antigen from a pathogenic virus, expression of the plurality of the antigen sequences eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not cause a malignancy naturally associated with the pathogenic virus in the host.

According to the embodiment, the recombinant virus may be any virus, preferably replication-incompetent adenovirus, adeno-associated virus, SV40 virus, retrovirus, herpes simplex virus or vaccinia virus. The recombinant virus may also preferably have the pathologic regions of the native progenitor of the benign virus deleted but retain its infectivity to the host.

Also according to the embodiment, the plurality of the antigen sequences may be multiple copies of the same antigen sequence or multiple antigen sequences that differ from each another.

In a variation of the embodiment, at least two of the plurality of the antigen sequences are expressed from a promoter bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

Alternatively, at least two of the plurality of the antigen sequences are expressed from a promoter to form a fusion protein.

Also according to the embodiment, the recombinant virus further comprises at least one promoter heterologous to the native progenitor of the recombinant virus that controls the expression of at least two of the plurality of

the antigen sequences. Examples of the promoter heterologous to the native progenitor of the recombinant virus include, but are not limited to, insulin promoter, CMV promoter and its early promoter, SV40 promoter, Rous sarcoma virus LTR promoter/enhancer, the chicken cytoplasmic β-actin promoter, and inducible promoters such as tetracycline-inducible promoter.

Also according to the embodiment, the plurality of antigen sequences may be a combination of antigens from at least two strains of the pathogenic virus.

Optionally, the plurality of antigen sequences may be a combination of antigens from at least two different pathogenic viruses. For example, the plurality of antigen sequences may be a combination of antigens from HIV-1, HIV-2, herpes simplex virus type 1, herpes simplexvirus type 2, Influenza virus, Marburg virus, Ebola virus, Arbovirus (a group of viruses carried by mosquitoes that cause encephalitis, yellow fever, and dengue), and hepatitis A, B, C, D, and E viruses.

In a variation of the embodiment, the viral genome of the recombinant virus may further comprise one or more immuno-stimulator sequences that is heterologous to the recombinant virus and encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen. For example, the immuno-stimulator may be a cytokine. Examples of the cytokine include, but are not limited to, interleukin-2, interleukin-4, interleukin-12, β-interferon, λ-interferon, γ-interferon, G-CSF, and GM-CSF.

According to the variation, the one or more immuno-stimulator sequences may be multiple copies of the same immuno-stimulator sequence or multiple immuno-stimulator sequences that differ from each other.

Optionally, at least two of the immuno-stimulator sequences may be expressed from a promoter bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism. Alternatively, at least two of the immuno-stimulator sequences may be expressed from a promoter to form a fusion protein.

The DNA sequence encoding viral antigen(s) is inserted into any non-essential region of the replication defective virus. In the case of adenovirus, for example, the nucleic acid is preferably inserted into the E1, E3 and/or E4 region of the adenovirus and most preferably into the E4 region. Because the

E1, E3 and E4 regions are available as insertion sites, the present invention also contemplates separate insertion of more than one encoding sequence.

In the recombinant viral vector vaccines of the present invention, the selected nucleotide sequences of the viral antigens are operably linked to control elements that direct transcription or expression thereof in the subject *in vivo*. Either homologous or heterologous viral control sequences can be employed. Useful heterologous control sequences generally include those derived from sequences encoding hostian or viral genes. Examples include, but are not limited to a cytomegalovirus (CMV) promoter such as the CMV immediate early promoter region (CMV_{ie}), SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (AdMLP), a herpes simplex virus promoter,and a retrovirus LTR promoter. Preferably, any strong constitutive promoter may be operatively linked to viral antigens or cytokines. More preferably the viral promoter is CMV immediate early promoter (CMV_{ie}).

Figures 1A-1C illustrate a method for constructing a recombinant adenoviral vector as a genetic vaccine of the present invention. The recombinant adenoviral vector of the present invention is constructed by using shuttle plasmids or vectors carrying multiple antigen genes and multiple cytokine genes.

Figure 1A illustrates a shuttle plasmid (pLAd.Antigen) containing two antigen genes, Antigen 1 and Antigen 2.. The shuttle plasmid pLAd.Antigen contains the left end of the adenoviral genome including the left long terminal repeats L-TR, and an adenoviral packaging signal (ψ). The E1 region of the adenovirus is replaced by a multiple gene expression cassette and CMV_{ie} promoter.

Genes encoding Antigen 1 and Antigen 2 are placed under the transcriptional control of the CMV_{ie} promoter by a splicing mechanism at the SD and SA sites. The plasmid pLAd.Antigen also contains a SV40 polyadenylation site, as well as prokaryotic replication origin and ampicillin-resistance gene for DNA propagation in bacteria.

Figure 1B illustrates another shuttle plasmid (pRAd.Cytokines) containing multiple cytokine genes such as IL-2, INF, and IL-8. The shuttle plasmid pRAd.Cytokines contains the right end of the adenoviral genome including the right long terminal repeats R-TR. Most of the E4 region (except

orf6) is replaced by the cytokine genes. Expression of cytokine genes is under the transcriptional control of the CMV_{ie} promoter via an internal ribosomal entry site (IRES) and by a splicing mechanism at the SD and SA sites. The plasmid pRAd.Cytokines also contains a bovine growth hormone (BGH) polyadenylation site, as well as a prokaryotic replication origin and ampicillin-resistance gene for DNA propagation in bacteria.

The recombinant adenoviral genome is assembled from the two shuttle plasmids, pLAd.Antigen and pRAd.Cytokines, which carries the left and right end of the adenoviral genome, respectively. The shuttle plasmids pLAd.Antigen and pRAd.Cytokines are digested with restriction enzymes such as XbaI and EcoRI, respectively.

As illustrated in **Figure 1C**, the fragments corresponding to the left end and right end of adenovirus from these two shuttle plasmids, pLAd.Antigen and pRAd.Cytokines, are isolated and ligated to the middle section of the adenoviral genome (the adenovirus backbone).

The ligated vector genome DNA is then transfected into 293HK cells that express the E1 proteins of adenovirus. In the presence of E1 proteins, the vector genome in which the E1 has been deleted can replicate and be packaged into viral particle, i.e. producing the recombinant adenoviral vector that can be used as a genetic vaccine of the present invention. The E1 region which is preserved in a native adenoviral genome but deleted from the recombinant viral genome is an example of the pathologic region native to the native progenitor of the recombinant virus: the wild type adenovirus.

Figure 5 illustrates an example of a genetic vaccine constructed by using the method described above. The replication defective adenovirus, type 5, is the vector backbone into which viral antigen and cytokines are inserted in the E1 region. The viral antigens are expressed using the CMVie promoter. The gene for the viral antigen is followed by the gene encoding INF-γ and GM-CSF, utilizing 2 IRES sequences to achieve expression of the three proteins from a single mRNA. IL2 and IL4 are controlled by a second CMV_{ie} promoter as a bi-cistronic cassette, followed by a second bi-cistronic cassette that express the two subunits of IL12 in the E4 region. Those skilled in the art will appreciate that the present invention is not limited to the structure discussed above, but that alternative cytokines may be used alone or in combination with

these and/or other cytokines. The detailed information about of these cytokines are described in the following section.

2. Cytokines Co-Expressed With Viral Antigens

The recombinant virus of the present invention may also express an immuno-stimulator to mimic cytokine-releasing response of a host cell upon viral infection and further augment immune response to the viral antigen co-expressed from the recombinant virus. The immuno-stimulator may be an immunoenhancing cytokine to further stimulate the immune system. The recombinant virus may encode one or multiple cytokines in any combination. Alternatively, multiple cytokines may be expressed by more than one recombinant virus or delivered to the host by using other techniques such as delivery via naked DNA plasmids or injection of cytokine proteins.

Examples of cytokine include, but are not limited to, interleukin-2, interleukin-4, interleukin-8, interleukin-12, β- interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor (G-CSF), and granulocyte-macrophage colony stimulating factor (GM-CSF).

Cytokines are immunodmodulatory molecules particularly useful in the vaccines of the invention as they are pleitropic mediators that modulate and shape the quality and intensity of the immune response. Cytokines are occasionally autocrines or endocrines, but are largely paracrine hormones produced in nature by lymphocytes and monocytes.

As used herein, the term "cytokine" refers to a member of the class of proteins or peptides that are produced by cells of the immune system and that regulate or modulate an immune response. Such regulation can occur within the humoral or the cell mediated immune response and includes modulation of the effector function of T cells, B cells, NK cells, macrophages, antigen-presenting cells or other immune system cells.

Cytokines are typically small proteins or glycoproteins having a molecular mass of less than about 30 kDa. As used herein the term cytokine encompasses those cytokines secreted by lyphocytes and other cell types (often designated as lymphokines) as well as cytokines secreted by monocytes and macrophages and other cell types (often designated as monokines). As used herein, the term cytokine encompasses those cytokines secreted by lymphocytes and other cell types as well as cyotkines secreted by

monocytes and macrophages and other cell types. The term cytokine includes the interleukins, such as IL-2, IL-4, IL-5, IL-8, IL-10, IL-11, IL-12, IL-15, and IL-18, which are molecules secreted by leukocytes that primarily affect the growth and differentiation of hematopoietic and immune system cells, and human proinflammatory cytokines such as IL-1a, TNF-a and TNF-b). The term cytokine also includes hematopoietic growth factors and, in particular, colony stimulating factors such as colony stimulating factor-1, granulocyte colony stimulating factor and granulocyte macrophage colony stimulating factor.

The cytokines can have the sequence of a naturally occurring cytokine or can have an amino acid sequence with substantial amino acid sequence similarity, e.g., 60-95% amino acid sequence similarity, preferably 70-98% amino acid sequence, and most preferably 75-95% amino acid sequence similarity to the sequence of a naturally occurring cytokine.

Thus, it is understood that limited modifications to a naturally occurring sequence can be made without destroying the biological function of the cytokine. For example, minor modifications of gamma interferon that do not destroy its function fall within the definition of gamma interferon. These modifications can be deliberate, as through site-directed mutagenesis, or can be accidental such as through mutation. The preferred cytokines are IL-2, IL-8, IL-12, or γ- interferon, β-Interferon, λ-interferon, GM-CSF, or G-CSF or a combination thereof.

Interleukin-2 is a lymphokine produced by helper T cells and is active in controlling the magnitude and type of the immune response. Smith, K. A., *Ann. Rev. Immunol.* 2, 319-333 (1984). Other functions have also been ascribed to IL-2 including the activation of NK cells (Minato, N. et al., *J. Exp. Med.* 154, 750 (1983)) and the stimulation of cell division in large granular lymphocytes and B cells. Tsudo, M. et al.. *J. Exp. Med.* 160, 612-616 (1984). Studies in mice and humans have demonstrated that deficient immune responsiveness both *in vivo* and *in vitro* can be augmented by IL-2. For example, exogenous IL-2 can restore the immune response in cyclophosphamide-induced immunosuppressed mice (Merluzzi, V. J. et al. *Cancer Res.* 41, 850-853 (1981)) and athymic (nude) mice. Wagner, H. et al. *Nature* 284, 278-80 (1982). Furthermore, IL-2 can restore responsiveness of lymphocytes from patients with various immunodeficiency states such as

leprosy and cancer. Vose, B. M. et al. *Cancer Immuno.* 13, 105-111 (1984). The genes for murine (Yokota, T. et al. *Proc. Natl. Acad. Sci. USA* 82, 68-72 (1985)) and human (Taniguchi, T. et al. *Nature*, 302, 305-307 (1983)) IL-2 have been cloned and sequenced.

Interleukin-4 is a T cell derived factor that acts as an induction factor on resting B cells, as a B cell differentiation factor and as a B cell growth factors. Sevenusar, E. Eur. J. Immunol. 17, 67-72 (1987). The gene for human IL-4 has been isolated and sequenced. Lee, F. et al. Proc. Natl. Acad. Sci. USA 83, 2061-2065 (1986).

IL-12 is a recently characterized heterodimeric cytokine that has a molecular weight of 75 kDa and is composed of disulfide-bonded 40 kDa and 35 kDa subunits. It is produced by antigen presenting cells such as macrophages, and binds to receptors on activated T, B and NK cells (Desai, B. B., et al., *J. Immunol.*, 148:3125-3132 (1992); Vogel, L. A., et al., *Int. Immunol.*, 8:1955-1962 (1996)). It has several effects including 1) enhanced proliferation of T cells and NK cells, 2) increased cytolytic activities of T cells, NK cells, and macrophages, 3) induction of IFN-□ production and to a lesser extent, TNF-α and GM-CSF, and 4) activation of TH1 cells. (Trinchieri, G., et al., *Blood*, 84:4008-4027 (1994). IL-12 has been shown to be an important costimulator of proliferation in Th1 clones (Kennedy et al., *Eur. J. Immunol.* 24:2271-2278 (1994)) and leads to increased production of IgG2a antibodies in serum (Morris, S. C., et al., *J. Immunol.* 152:1047-1056 (1994); Germann, T. M., et al., Eur. *J. Immunol.*, 25:823-829 (1995); Sher, A., et al., *Ann. N.Y. Acad. Sci.*, 795:202-207 (1996); Buchanan, J. M., et al., *Int. Immunol.*, 7:1519-1528 (1995); Metzger, D. W. et al., *Eur. J. Imunol.*, 27:1958-1965 (1997)). Administration of IL-12 can also temporarily decrease production of IgG1 antibodies (Morris, S. C., et al., *J. Immunol.* 152:1047-1056 (1994); McKnight, A. J., *J. Immunol.* 152:2172-2179 (1994); Buchanan, J. M., et al., *Int. Immunol.*, 7:1519-1528 (1995)), indicating suppression of the Th2 response. The purification and cloning of IL-12 are disclosed in WO 92/05256and WO 90/05147, and in EP 322,827 (identified as "CLMF"). All of the above effects were observed in adult animals.

Interferons (IFNs) are relatively small, species-specific, single chain polypeptides, produced by hostian cells in response to exposure to a variety of inducers such as viruses, polypeptides, mitogens and the like. They exhibit

antiviral, antiproliferative and immunoregulatory properties and are, therefore, of great interest as therapeutic agents in the control of cancer and various other antiviral diseases (J. Desmyter et al., *Lancet* 11, 645-647 (1976); R. Derynck et al., *Nature* 287, 193 (1980)). Human interferons are grouped into three classes based on their cellular origin and antigenicity: α-interferon (leukocytes), β-interferon (fibroblasts) and γ-interferon (B cells). Recombinant forms of each group have been developed and are commercially available.

γ-interferon is also a T cell derived molecule which has profound effects on the immune response. The molecule promotes the production of immunoglobulin by activated B cells stimulated with interleukin-2. γ-interferon also increases the expression of histocompatability antigens on cells which associated with viral antigens to stimulate cytotoxic T cells. The gene for human γ-interferon has been isolated and sequenced. Gray, P. W. et al., *Nature* 295, 503-508 (1982).

Human alpha interferons (also known as Leukocyte Interferons) comprise a family of about 30 protein species, encoded by at least 14 different genes and about 16 alleles. Some of these alpha interferon protein species have been shown to have antiviral, antigrowth and immunoregulatory activities. *See, e.g.*, Pestka et al., *Ann. Rev. Biochem.*, 56:727 (1987). The therapeutic efficacy of human alpha interferons has been established for human cancers and viral diseases. For example, recombinant interferons (IFN alpha-2a, IFN alpha-2b, IFN alpha-2c), cell-line derived interferon (IFN alpha-n1) and interferon derived from leukocytes (IFN alpha-n3) are currently used for the treatment of Condyloma acuminata, hepatitis (Weck et al., *Am. J. Med.*, 85(Suppl 2A):159 (1988); Korenman et al., *Annal. Intern. Med.*, 114.:629 (1991); Friedman-Kien et al., *JAMA*, 259:533 (1988)), for the regression of some malignancies (Baron et al., *JAMA*, 266:1375 (1991)), for the treatment of AIDS related Kaposi's sarcoma (Physicians Desk Reference, 47th edit., eds. Medical Economics Data, Montvale, N.J., p. 2194 and 2006 (1993)) and are currently being considered for the treatment of human acquired immunodeficiency syndrome (AIDS) either alone or in combination with other antiviral agents (Hirsch, *Am. J. Med.*, 85(Suppl 2A):182 (1988)).

β-interferon has been shown to be a glycoprotein by chemical measurement of its carbohydrate content. It has one N-glycosidyl attachment

site (E. Knight, Jr., *Proc. Natl. Acad. Sci.*, 73, 520 (1976); E. Knight, Jr., and D. Fahey, *J. Interferon Res.*, 2 (3), 421 (1982)). Even though not much is known about the kinds of sugars which make up the carbohydrate moiety of β-interferon, it has been shown that the carbohydrate moiety is not essential for its antigenicity, biological activity or hydrophobicity (T. Taniguchi et al., supra; E. Knight, Jr., supra; and E. Knight, Jr. and D. Fahey, supra). Beta-interferon can be induced in fibroblasts by viral challenge and contains about 165 amino acids. The sequence of □-interferon is known. Fiers et al. *Philos. Trnas. R. Soc. Lond., B, Biol. Sci.* 299:29-38 (1982).

GM-CSF is a cytokine important in the maturation and function of dendritic cells. It binds receptors on dendritic cells and stimulates these cells to mature, present antigen, and prime naive T cells. Dendritic cells form a system of highly efficient antigen-presenting cells. After capturing antigen in the periphery, dendritic cells migrate to lymphoid organs and present antigens to T cells. These potent antigen-presenting cells are unique in their ability to interact with active naive T cells. The potent antigen-presenting capacity of dendritic cells may be due in part to their unique life cycle and high level expression of major histocompatibility complex class I and II molecules and co-stimulatory molecules. The sequence of human GM-CSF is known. Wong et al., *Science* 228:810-815 (1985).

Granulocyte colony stimulating factor (G-CSF) is one of the hematopoletic growth factors, also called colony stimulating factors, that stimulate committed progenitor cells to proliferate and to form colonies of differentiating blood cells. G-CSF preferentially stimulates the growth and development of neutrophils, and is useful for treating in neutropenic states. Welte et at., *PNAS-USA* 82: 1526-1530 (1985); Souza et at., *Science* 232: 61-65 (1986) and Gabrilove, J. *Seminars in Hematology* 26: (2) 1-14 (1989). G-CSF increases the number of circulating granulocytes and has been reported to ameliorate infection in sepsis models. G-CSF administration also inhibits the release of tumor necrosis factor (TNF), a cytokine important to tissue injury during sepsis and rejection. See, e.g., Wendel et al., *J. Immunol.*, 149:918-924 (1992). The cDNAs for human (Nagata et al., *Nature* 319;415, 1986) and mouse G-CSF (Tsuchiya et al., *PNAS* 83, 7633, 1986) have been isolated, permitting further structural and biological characterization of G-CSF.

In humans, endogenous G-CSF is detectable in blood plasma. Jones et al., *Baillière's Clinical Hematology* 2 (1): 83-111 (1989). G-CSF is produced by fibroblasts, macrophages, T cells trophoblasts, endothelial cells and epithelial cells and is the expression product of a single copy gene comprised of four exons and five introns located on chromosome seventeen. Transcription of this locus produces a mRNA species which is differentially processed, resulting in two forms of G-CSF mRNA, one version coding for a protein of 177 amino acids, the other coding for a protein of 174 amino acids. Nagata et at., *EMBO J* 5: 575-581 (1986). The form comprised of 174 amino acids has been found to have the greatest specific *in vivo* biological activity. G-CSF is species cross-reactive, such that when human G-CSF is administered to another host such as a mouse, Canine or monkey, sustained neutrophil leukocytosis is elicited. Moore et at. *PNAS-USA* 84: 7134-7138 (1987).

The present invention provides an effective means for enhancing the immune response to the specific foreign antigenic polypeptides of recombinant viruses. Although any foreign antigenic polypeptide can be used in the vaccine of the present invention, the vaccine is particularly useful in vaccines against the HIV virus and the Ebola virus, since these viruses have a negative effect on the host's immune system. The vaccine is also very useful for immunization against hepatitis B and C virus.

3. Genetic Vaccines Against HIV Infection

The genetic vaccine of the present invention also addresses the need for an efficient vaccine against the HIV virus. According to the present invention the genetic vaccine may be a recombinant benign virus in which the viral genome carries one or more antigens from HIV, such as HIV glycoproteins (e.g. GP120 and GP41) or capsid proteins (e.g. P24). Sequences of these HIV antigens may be modified such as deletion of the immunosuppressive regions of the HIV glycoproteins.

The HIV virus causes the disease known as Acquired Immune Deficiency Syndrome (AIDS). AIDS has been described as a modern plague since its first description in 1981, it has claimed over 60,000 victims, and accounted for over 32,000 deaths in the United States alone. The disease is characterized by a long aysmptomatic period followed by a progressive

degeneration of the immune systemand the central nervous system. The virus may remain latent in infected individuals for five or more years before symptoms appear, and thus, the true impact of the disease has yet to be felt. Many Americans may unknowingly be infected and capable of infecting others who might come into contact with their body fluids. Thus, if unchecked, the personal, social and economic impact of AIDS will be enormous.

The HIV virus is a retrovirus. Thus, its genetic matierial is RNA, which encodes the information for viral replication. Upon infection of a host cell, the RNA acts as a template for the transcription to DNA, which is catalyzed by an enzyme called reverse transcriptase. The DNA so produced enters the cell nucleus where it is integrated into the host DNA as a provirus. When properly activated, the retroviral-derived DNA is transcribed and translated to produce RNA containing virions, which are then released from the cell by a budding process.

When an individual becomes infected with HIV, the virus preferentially attaches to and enters a particular class of white blood cells, called T4 lymphocytes, which are characterized by the presence of a cell surface marker termed CD4. These white blood cells play an integral role in the immune system, functioning as critical components of both the humoral and cellular immune response. Much of the deleterious effect of HIV can be attributed to the functional depression or destruction of T4 lymphocytes.

The intact HIV virion is roughly spherical and is approximately110 nm in diameter. The virion has an outer membrane covered with spike-like structures made up of glycoprotein, gp160/120. In addition, there exists a transmembrane protein termed gp41. Inside the virion are two structural proteins: an outer shell composed of the phosphoprotein, p17, and an inner nucleoid or central core made up of the phosphoprotein, p24. The viral RNA is present inside the core along with two copies of the reverse transcriptase enzyme, p66/51, which is necessary for the synthesis of viral DNA from the RNA template. The HIV RNA genome encodes three major structural genes: gag, pol and env, which are flanked at either end by long terminal repeat (LTR) sequences. The gag gene codes for the group-specific core proteins, p55, p39, p24, p17 and p15. The pol genes code for the reverse transcriptase, p66/p51, and the protease, p31. The env genes encode the outer envelope glycoprotein, gp120, and its precursor, gp160, and the

transmembrane glycoprotein, gp41. Some of the genes tend to be highly variable, particularly the env genes. In addition, there are five other genes, not shared by other retroviruses, which are either involved in transcriptional or translational regulation or encode other structural proteins. The entire HIV genome has now been sequenced. See Ratner et al. Nature 313:277 (1985), which is incorporated herein by reference.

The HIV envelope protein has been extensively described, and the amino acid and RNA sequences encoding HIV envelope from a number of HIV strains are known. See Myers, G. et al., *Human Retroviruses and AIDS: A compilation and analysis of nucleic acid and amino acid sequences*, Los Alamos National Laboratory, Los Alamos, N.M. (1992). The *env* genes of various strains of HIV are predicted to encode proteins of 850 to 880 amino acids. Extensive glycosylation of the Env precursor polyprotein during synthesis produces gp160 (about 160 kilodaltons) which is also the major form of the *env* gene product detected in infected cells. Gp160 forms a homotrimers and undergoes glycosylation with the Golgi apparatus.

The functional domains of gp160 includes, starting from N-terminus, Signal peptide, Variable regions 1 through 5 which encompass CD4 binding sites (e.g., Thr^{257}, Trp^{427}, Asp^{368}/Glu^{370}, and Asp^{457}), Proteolytic processing site (also called the cleavage site between gp120 and gp41), Fusion domain, Leucine zipper motif, transmembrane domain, and Lentivirus lytic peptides (LLP) 1 and 2. Although the nucleotide and amino acid sequences of gp120 and the numbering thereof from various isolates and strains of HIV may differ, the region encoding the functional domains can be readily identified by the teaching in Luciw (1996) in "Fundamental Virology", 3rd ed., eds., Fields et al., Lippincott-Raven Publishers, Philadelphia, Chapter 27, pp. 845-916.

The signal peptide at the N-terminus of the Env precursor gp160 directs ribosomes translating the nascent protein to the endoplasmic reticulum; an intracellular proteinase removes this signal peptide during Env gp biogenesis. The Env precursor gp160 is cleaved at the processing site by a cellular protease to produce gp120 (designated SU subunit) and gp41 (designated TM subunit). Gp120 contains most of the external, surface-exposed, domains of the envelope glycoprotein complex. Gp41 contains a transmembrane domain and remains in a trimeric configuration, and it interacts with gp120 in a non-covalent manner. The subunits of gp41 include:

Fusion peptide, Leucine zipper-like region, transmembrane domain (TM), LLP1 and LLP2.

The gp120 subunit contains five variable regions and six conserved regions. The variable (V) domains and conserved (C) domains of gp120 are specified according to the nomenclature of Modrow et al. (1987) "Computer-assisted analysis of envelope protein sequences of seven human immunodeficiency virus isolates: predictions of antigenic epitopes in conserved and variable regions", J. Virol. 61:570-578.

The gp120 molecule consists of a polypeptide core of 60,000 daltons, which is extensively modified by N-linked glycosylation to increase the apparent molecular weight of the molecule to 120,000 daltons. The positions of the 18 cysteine residues in the gp120 primary sequence, and the positions of 13 of the approximately 24 N-linked glycosylation sites in the gp120 sequence are common to all gp120 sequences. The hypervariable domains contain extensive amino acid substitutions, insertions and deletions. Sequence variations in these domains result in up to 30% overall sequence variability between gp120 molecules from the various viral isolates. Despite this variation, all gp120 sequences preserve the virus's ability to bind to the viral receptor CD4 and to interact with gp41 to induce fusion of the viral and host cell membranes.

The HIV virus attaches to host cells by an interaction of the envelope glycoproteins with a cell surface receptor. It appears that when HIV makes contact with a T4 cell, gp120 interacts with the CD4 receptor. Recently, the crystal structure of the core domain of HIV-1 gp120 (strain HXB-2, a clade B virus) has been solved by complexing the protein with a fragment of human CD and an antigen-binding fragment from a virus-neutralizing antibody that blocks chemokine-receptor binding. Kwong et al. (1998) "Structure of an HIV gp120 envelope glycoprotein in complex with the CD4 receptor and a neutralizing human antibody", Nature 393:648-659. These studies revealed that the gp120 core has a unique molecular structure that comprises two domains—an "inner domain" (which faces gp41) and an "outer" domain (which is mostly exposed on the surface of the oligomeric envelope glycoprotein complex). The two gp120 domains are separated by a "bridging sheet" that is not part of either domain. Binding to CD4 causes a conformational change in gp120 which exposes the bridging sheet and may move the inner and outer

domains relative to each other. It was also found that most of the carbohydrate molecules which are added to gp120 are added to the outer domain. This is consistent with the idea that that virus uses carbohydrate molecules to mask external antigenic epitopes on gp120.

Gp120 not only binds to the cellular CD4 receptor but also to HIV coreceptors such as the cellular chemokine receptors (e.g. CCR5). Upon binding to the receptor and/or coreceptor, the viral envelope is then fused with the cell membrane and the inner core of the virus enters the infected cell where the transcription of RNA into a DNA provirus is catalyzed by reverse transcriptase. The provirus may remain in the cell in a latent form for some months or years, during which time the infected individual is asymptomatic. However, if the virus is later activated causing viral replication and immuno-suppression the individual will than be susceptible to the opportunistic infections associated with AIDS.

In one embodiment of the HIV vaccine of the present invention, a recombinant virus is provided for eliciting strong immune response against infection of HIV. The recombinant virus comprises: an antigen sequence heterologous to the recombinant virus that encodes an antigen from human immunodeficiency virus (HIV), expression of the HIV antigen eliciting an immune response directed against the HIV antigen and cells expressing the HIV antigen in a host upon infection of the host by the recombinant virus; and an immuno-stimulator sequence heterologous to the recombinant virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the HIV antigen. In a preferred embodiment, the recombinant virus is replication-incompetent and does not cause a malignancy naturally associated with HIV in the host. The recombinant virus is used as a genetic vaccine to be administered to a host to induce or elicit strong and long-lasting immunity against HIV infection.

In comparison with other approaches for developing HIV vaccine using denatured or attenuated HIV virion, the approach of the present invention should be safer and more efficient in eliciting strong immune response but not creating risks of reactivation of HIV, probably through recombination with the wild type HIV infecting the host.

According to the present invention, the HIV antigen expressed by the genetic vaccine may be any antigen derived from a HIV virus, such as HIV

surface, core/capsid, regulatory, enzyme and accessory proteins. Examples of HIV surface protein include, but are limited to the products of the *env* gene such as gp120 and gp41. Examples of HIV capsid protein include, but are limited to the products of the *gag* gene such as the cleavage products of the $Pr55^{gag}$ by the viral encoded protease PR: the mature capsid proteins MA (p17), CA (p24), p2, NC (p7), p1 and p6. Herderson et al. (1992) J. Virol. 66:1856-1865. Examples of viral regulatory proteins include, but are not limited to the products of the *tat* and *rev* genes: Tat and Rev. Examples of viral enzyme proteins include, but are not limited to the products of the *pol* gene: p11 (protease or PR), p51 (reverse transcriptase or RT), and p32 (integrase or IN). Examples of viral accessory proteins include, but are not limited to the products of the *vif, vpr, vpx, vpu* and *nef* genes: Vif, Vpr, Vpx, Vpu and Nef.

In one embodiment, HIV Nef protein may serve as the HIV antigen expressed by the recombinant virus of the present invention. For example, sequence encoding Nef (e.g., the *nef* sequence at position 8152-8523 for BH10 strain of HIV and at position 8787-9407 for pNL4-3 strain of HIV) may be inserted into the vector.

In another embodiment, HIV Rev protein may serve as the HIV antigen expressed by the recombinant virus of the present invention. For example, sequence encoding Rev (e.g., the *rev1* sequence at position 5969-6044 and the *rev2* sequence at position 8369-8643 for pNL4-3 strain of HIV) may be inserted into the vector.

In yet another embodiment, full length HIV Gag protein may serve as the HIV antigen expressed by the recombinant virus of the present invention. For example, sequence encoding full length Gag (e.g., the *gag* sequence at position 112-1650 for BH10 strain of HIV and at position 790-2292 for pNL4-3 strain of HIV) may be inserted into the vector.

Alternatively, capsid protein from HIV Gag protein (e.g. p24 CA) may serve as the HIV antigen expressed by the recombinant virus of the present invention. For example, sequence encoding p24CA (e.g., the sequence at position 1186-1878 for BH10 strain of HIV and at position 508-1200 for pNL4-3 strain of HIV) may be inserted into the vector.

In yet another embodiment, the HIV antigen expressed by the recombinant virus is derived from the *env* gene products. For example, the antigen is derived from the Env protein.

According to the embodiment, modifications or mutagenesis may be used to delete or mutate in certain region(s) of Env to render it non-functional and yet still contains neutralizing epitopes for its natural genicity. For example, the proteolytic processing site of Env may be deleted or mutated to render it resistant to cleavage by cellular protease to produce gp120 and gp41 fragments. Deletion or mutation may also be carried out on the transmembrane and cytoplasmic domains of gp41 such as the TM, LLP-1 and LLP-2 domains. Compared to the wild type Env, the mutated Env protein should have a reduced risk of being incorporated into a wild type HIV that infects the host and being exploited by HIV in its furtherance of the goal: destruction the host's immune system.

For example, wildtype HIV Env can be modified in the following ways. Wildtype gp120 sequence from BH10 strain of HIV and containing Env, Tat, and Rev coding sequences can be digested with restriction enzymes EcoR I and Xho I to produce a fragment starting from nucleotide 5101 and ending at nucleotide 8252. The cytosolic domain of Env can be removed by deleting nucleotides from the coding sequence at position 7848-8150 for BH10 strain, and 8610-8785 for pNL4-3 strain of HIV. The cleavage site of Env can be removed by deleting 12 nucleotides encoding amino acid sequence REKR at position 7101-7112 for BH10 strain, and 7736-7747 for pNL4-3 strain of HIV.

Also according to this embodiment, the modified Env protein may contain deletions in the regions that do not contain neutralizing epitopes. For example, the V1 and V5 domains of gp120 may be deleted without sacrificing the natural antigenicity of gp120. Portions of the V2 and V3 domains of gp120 that do not contain neutralizing epitopes may also be deleted. Although the principle neutralizing domain (PND) has been found in the V3 domain, V2 and C4 domains of gp120 have also been found to contain neutralizing epitopes. Among various strains or clades of HIV, the amino acid sequences of the neutralizing epitopes may be variable. However, it has been found that the amount of variation is highly constrained. Thus, the sequences not containing the neutralizing epitopes should be readily determined.

For example, sequence encoding V1 region of Env can be deleted at position 5961-6032 for BH10 strain, and 6602-6673 for pNL4-3 strain of HIV. Sequence encoding V2 region of Env can be deleted at position 6060-6161 for BH10 strain, and 6700-6796 for pNL4-3 strain of HIV. Optionally, sequence encoding both V1 and V2 regions of Env can be deleted at position 5961-6161 for BH10 strain, and 6602-6796 for pNL4-3 strain of HIV.

Alternatively, the HIV antigen expressed by the recombinant virus may be a subunit of gp120 which contains one or more selected variable (V) and/or conserved (C) domains. For example, the HIV antigen may be a gp120 subunit containing V2, V3 and C4 domains, or V3 and C4 domains. The location of neutralizing epitopes in the V3 domain is well known. It has been found that neutralizing epitopes in the V2 and C4 domains are located between residues 163 and 200 and between about 420 and 440, respectively. In addition, residues for antibody binding also include residues 171, 174, 177, 181, 183, 187, 188 in the V2 domain and residues 429 and 432 in the C4 domains. Berman et al. (1999) Virology 265:1-9; and Berman (1998) AIDS Res. Human Retroviruses 15:115-132.

In another embodiment, the HIV antigen expressed by the recombinant virus of the present invention may be a modified Env protein that contains deletions and/or mutations in the glycosylation sites. The gp120 of HIV-1 contains 24 potential sites for N-linked glycosylation (Asn-X-Ser/Thr); about 13 of the 24 glycosylation motifs are conserved in the different viral isolates. Analysis of HIV-1 Env gp proteins has demonstrated that 17 of 24 potential glycosylation sites are modified with carbohydrate side chains. Mizuochi et al. (1990) J. Biol. Chem. 265:8519-8524; and Leonard et al. (1990) J. Biol. Chem. 265:10373-10382. Because of the extensive glycosylation of Env gp proteins, very few regions of the peptide backbone of gp120 protrude from the carbohydrate mass. Some of the glycosylation sites have been found in non-neutralizing epitopes that dilute the immunity against true neutralizing epitopes or serve as decoy epitopes. Thus, deletion or mutation of these glycosylation sites may enhance immunity of the antigen by unmasking the true neutralizing epitopes.

In another embodiment, the different HIV antigens may be expressed by the same recombinant virus of the present invention. For example, both Env, Tat and Rev proteins may be expressed from the same promoter such as

a CMV early promoter via a retroviral splicing donor-acceptor mechanism. Optionally, HIV Gag protein, either in full length or a truncated or modified form (e.g., capsid protein p24), may also be expressed together with other HIV antigens such as Env, Tat and Rev. Further, these HIV antigens may be expressed together with the immuno-stimulator(s) (e.g., IL-2, IL-12, INF-γ, and GMCSF) in single or multiple copies by the same recombinant viral vector.

For example, the sequences encoding the HIV antigens may be inserted into E1 region of an adenoviral vector and expressed from a CMV early promoter via a retroviral splicing donor-acceptor mechanism or an IRES mechanism. The sequences encoding the immuno-stimulators may be inserted into E4 region of the same adenoviral vector and expressed from another CMV early promoter via a retroviral splicing donor-acceptor mechanism or an IRES mechanism.

In yet another embodiment, the sequence encoding the HIV antigen in the recombinant virus of the present invention is a mosaic antigen that contains sequences from different strains, isolates and/or clades of HIV viruses. A strain of HIV is the HIV isolated from an individual (an isolate), characterized and given a strain name (e.g., MN, LAI). Because of the heterogenecity of HIV, not two isolates are exactly the same. A group of related HIV isolates are classified according to their degree of genetic similarity such as of their envelop proteins. There are currently two groups of HIV-1 isolates, M and O. The M group consists of at least 9 clades (also called subtypes), A through I. The O group may consist of a similar number of clades. Clades are genetically distinct but are all infectious. It is believed that by using a mosaic HIV antigen in the design of the genetic vaccine of the present invention the vaccine produced should have an enhanced ability to stimulate the production of anti-HIV antibodies and HIV-specific cytotoxic T lymphocytes (CTLs) against a wider spectrum of "wild type" HIV strains.

In one embodiment, the mosaic HIV antigen in the recombinant virus contains antigens from multiple clades of HIV-1, including clade A (Accession No: HIV-1 92UG037WHO.0108HED), B (Accession No: pNL4-3), C (Accession No: HIV-1 92BR025WHO.109HED), D (Accession No: HIV-1 92UG024.2), E (Accession No: HIV-1 93TH976.17), F (Accession No: HIV-1 93BR020.17), and G (Accession No: HIV-1 92RU131.9). Optionally, multiple repeats of restriction fragments of HIV antigen (e.g., Ava I fragments) from

different clades may be linked head-to-tail to generate an even more complex mosaic HIV antigen.

For example, an adenoviral vector may be constructed to the V3 loops of multiple clades as the mosaic HIV antigen. Optionally, HIV antigens with gp41 deletion from multiple clades may serve as the mosaic HIV antigen. Alternatively, HIV antigens from multiple clades with V1 and V2 loops deleted from clade B (pNL4-3) may serve as the mosaic HIV antigen.

Yet optionally, a human gene Thy-1 GPA anchor sequence encoding amino acid sequence SWLLLLLLSLSLLQATDFMSL [SEQ ID NO: 9] may be added to the recombinant viral construct.

In another embodiment, the mosaic HIV antigen contains an Env protein which comprises variable and constant domains of gp120 derived from different strains, isolates and/or clades of HIV viruses. For example, V2 domain from clade B of the M group may be mixed with V3 and C4 domains from clade C of the O group to generate a mosaic HIV antigen. Vaccination of individuals with such a mosaic antigen may stimulate CTLs with cross-clade activity. In another word, these CTLs can recognize and kill target cells infected HIV from different clades.

Alternatively, the recombinant virus may express a plurality of HIV antigens, each of which is an antigen from a different strain, isolate or clade of HIV. For example, *env* genes from different clades of HIV can be cloned into the recombinant virus and expressed in tandem to produces various Env proteins from these clades in the host cells. It is believed that expressing various Env proteins from different strains, isolates or clades of HIV in the host cells should enhance the ability of the genetic vaccine of the present invention to stimulate the production of anti-HIV antibodies and HIV-specific cytotoxic T lymphocytes (CTLs) against a wider spectrum of "wild type" HIV strains. The host vaccinated with such a vaccine would be able to be immunized from infection of various strains of HIV.

By using the genetic vaccine of the present invention, individuals not infected by HIV may be immunized against HIV. For HIV-infected individuals the vaccine may also be used boost their immune response and help fight against this virulent virus. Since the genetic vaccine can express high level of antigens and/or a variety of HIV glycoproteins and capsid proteins simultaneously, the vaccinated individuals should be immunized against

various strains of HIV, such as HIV-1 and HIV-2. Additionally, since the genetic vaccine can express high levels of cytokines to mimic the body's response to natural viral infection, the body's immune response to such a genetic vaccine against HIV should be strong and long-lasting, thereby achieving a life-long immunity against this deadly virus.

4. Genetic Vaccines Against Hepatitis Viruses

The genetic vaccine of the present invention also addresses the need for an efficient vaccine against hepatitis viruses such as hepatitis A, B, C, D, and E viruses. According to the present invention the genetic vaccine may be a recombinant benign virus in which the viral genome carries one or more antigens from a hepatitis virus, such as glycoproteins and core proteins of the hepatitis virus. Sequences of these HIV antigens may be modified such as deletion of the pathogenic regions of the hepatitis glycoproteins or coreproteins.

In particular, the recombinant virus of the present invention can be used as a vaccine to immunize individuals against Hepatitis B infections. Viral hepatitis B is caused by the Hepatitis B virus (HBV). HBV is estimated to have infected 400 million people throughout the world, making HBV one of the most common humanpathogens. Hepatocellular carcinomas (HCC), one of the most common cancers afflicting humans, is primarily caused by chronic HBV infection.

HBV is a mostly double-stranded DNA virus in the *Hepadnaviridae* family. The HBV genome is unique in the world of viruses due to its compact form, use of overlapping reading frames, and dependence on a reverse-transcriptase step, though the virion contains primarily DNA. The HBV genome has four genes: pol, env, pre-core and X that respectively encode the viral DNA polymerase, envelope protein, pre-core protein (which is processed to viral capsid) and protein X. The function of protein X is not clear but it may be involved in the activation of host cell genes and the development of cancer.

The diagnosis of HBV infection is generally made on the basis of serology. Virtually all individuals infected with HBV will have detectable serum hepatitis surface antigens (HBsAg). Despite notable successes of vaccines against HBV infection, it is still an on-going task. A review on modern hepatitis

vaccines, including a number of key references, may be found in the Eddleston, *The Lancet*, p. 1142, May 12, 1990. *See also Viral Hepatitis and Liver Disease*, Vyas, B. N., Dienstag, J. L., and Hoofnagle, J. H., eds., Grune and Stratton, Inc. (1984) and *Viral Hepatitis and Liver Disease*, Proceedings of the 1990 International Symposium, eds F. B. Hollinger, S. M. Lemon and H. Margolis, published by Williams and Wilkins. According to the present invention, the viral antigen may be a surface antigen or core protein of hepatitis B virus such as the small hepatitis B surface antigen (SHBsAg) (also referred to as the Australia antigen), the middle hepatitis B surface antigen (MHBsAg) and the large hepatitis B surface antigen (LHBsAg).

Antigens of different types of HBV, such as Asian type C and America type A, may be expressed by the recombinant virus to elicit immune response to these types of HBV. The HBV surface antigen (HBsAg) or the core antigen (HBcAg) may be expressed by the recombinant virus of the present invention, separately or in combination (HBsAg + HBcAg).

For example, the sequences encoding multiple HBV antigens may be inserted into E1 or E4 region of an adenoviral vector and expressed from a CMV early promoter via a retroviral splicing donor-acceptor mechanism or an IRES mechanism. Further, these HBV antigens may be expressed in combination with one or more immuno-stimulators such as IL-2, IFN-γ and GMCSF in single or multiple copies. Sequences encoding these cytokines may be inserted into E4 or E1 region that is not occupied by the antigen sequences and expressed from another CMV early promoter via a retroviral splicing donor-acceptor mechanism or an IRES mechanism.

Specific combinations of inserts include, but are not limited to, HBsAg + HBcAg; HBsAg + HBcAg + IL-2; HBsAg + HBcAg + IFN-γ + GMCSF; and HBsAg + IFN-γ + IFN-γ + GMCSF.

The sequences encoding the immuno-stimulators may be inserted into E4 region of the same adenoviral vector and expressed from another CMV early promoter via a retroviral splicing donor-acceptor mechanism or an IRES mechanism.

Also according to the present invention, the viral antigen may be a surface antigen or core protein of hepatitis C virus such as NS3, NS4 and NS5 antigens.

For example, sequence(s) encoding the HCV antigen(s) may be inserted into E1 or E4 region of an adenoviral vector and expressed separately or in combination with one or more immuno-stimulators such as IL-2, IL-12, IFN-γ and GMCSF in single or multiple copies.

Specific combinations include, but are not limited to,

(1) HCV wildtype E2 + wildtype E1;

(2) core of HCV;

(3) HCV E2 + E1 + core;

(4) HCV E2 + E1 + core + IL-2;

(5) HCV E2 + E1 + core + IL-2 + IFN-γ + GMCSF; and

(6) HCV E2 + E1 + core + IL-2 + IFN-γ + IL-12.

In another embodiment, multi copies of hypervariable regions (HVR) of HCV E1 and E2, e.g., five copies of HVR (5xHVR), may serve as the viral antigen in the recombinant virus, and may be expressed alone or in combination with one or more immuno-stimulators such as IL-2, IL-12, IFN-γ and GMCSF in single or multiple copies.

Specific combinations include, but are not limited to,

(1) E2-5xHVR + E1;

(2) E2-5xHVR + E1 + IL-2;

(3) E2-5xHVR + E1 + core + IL-2;

(4) E2-5xHVR + E1 + core + IL-2 + IFN-γ + GMCSF; and

(5) E2-5xHVR + E1 + core + IL-2 +IL-12.

By using the genetic vaccine of the present invention, non-hepatitis-infected individuals may be immunized against hepatitis virus. For hepatitis virus-infected individuals the vaccine may also be used boost their immune response and help fight against the hepatitis virus. Since the genetic vaccine can express high level of antigens and/or a variety of hepatitis glycoproteins and coreproteins simultaneously, the vaccinated individuals should be immunized against various strains and/or types of hepatitis virus, such as hepatitis A, B, C, D, and E virus. Additionally, since the genetic vaccine can express high levels of cytokines to mimic the body's response to natural viral infection, the body's immune response to such a genetic vaccine against

hepatitis should be strong and long-lasting, thereby achieving a life-long immunity against the hepatitis virus.

5. Genetic Vaccines Against Ebola Virus

The genetic vaccine of the present invention also addresses the need for an efficient vaccine against the deadly virus, Ebola virus. According to the present invention the genetic vaccine may be a recombinant benign virus in which the viral genome carries one or more antigens from Ebola hepatitis, such as glycoproteins (e.g. GP1 and GP2) of Ebola virus. Sequences of these Ebola antigens may be modified such as deletion of the immunosuppressive regions and/or other pathogenic regions of the Ebola virus.

Ebola virus is one of the most lethal viruses known to mankind with a mortality rate of up to 90%. Johnson, K.M., *Ann Intern Med* 91(1):117-9 (1979). Victims of Ebola virus infection are subjected to a horrible hemorrhagic diseases which kills in a matter of days. The natural reservoir of the virus remains unknown, as do the specifics of pathogenesis of the infection. The virus has a very specific tropism for liver cells and cells of the reticuloendothelial system, such as macrophages. Massive destruction of the liver is hallmark feature of the disease.

Although Ebola virus infection is rare, there is concern by public health officials about the potential for the disease to become an international epidemic as the Ebola virus is easily transmitted through human contact and is extremely contagious. Outbreaks like those that have recently occurred in Africa could happen in industrialized countries due to the rapid and extensive nature of modern travel. Recent cases of Ebola virus infection in Africa send strong warnings to be prepared for the outbreaks of this extremely dangerous infectious disease. In addition, Ebola virus has a terrifying potential if used as a biological weapon by terrorist nations or organizations. As in most cases of viral infection, the best approach to prevent an outbreak of Ebola virus is through vaccination. However, currently there is no effective vaccine nor treatment available against Ebola virus infection.

Ebola viruses are enveloped, negative strand RNA viruses, which belong to the family Filoviridae. There are three strains of filoviruses: Ebola, Marburg and Reston. The Ebola virus can enter the body a number of different ways such as an opening through which air is taken in because the

virus can travel on airborne particles and it can also enter the body through any opening in the skin, such as cuts.

The Ebola virus has a non-segmented RNA genome that encodes all the viral structural proteins (nucleoprotein, matrix proteins VP24 and VP40), non-structural proteins (VP30, VP35) and viral polymerase. Peters, C.J., *West J Med*164(1):36-8 (1996). Among the viral proteins, the envelope glycoproteins (GP) exist in two forms, a secreted glycoprotein (50-70 kDa) and a transmembrane glycoprotein (130-170 kDa) generated by transcriptional editing. Sanchez, A. et al., *Proc Natl Acad Sci U.S.A.*, 93(8):3602-7 (1996). Although the two forms of GP share 295 amino acid homology, they have distinct binding specificities, suggesting that they play different roles in the course of viral infection. The secreted glycoprotein (sGP) is the predominant form synthesized and secreted by the infected cells. It may play a role in suppressing the host immune system (Yang,Z., et al., *Science* 279(5353):1034-7 (1998)) and may serve as a decoy to allow the virus particle to escape from neutralizing antibodies, since the two forms of GPs partly share their antigenicity. Analysis of monoclonal antibodies from the human survivors of Ebola virus Zaire infection has revealed that the vast majority of them were specific to the sGP, and only a few bound weakly to GP. Maruyama, T., et al., *J Infect Dis*, 179 Suppl 1:S235-9 (1999), Maruyama, T., et al., *J Virol*, 73(7):6024-30 (1999). Although the exact mechanism by which the sGP may suppress the immune system is not clearly understood, the large amounts of sGP synthesized in the early phase of the infection are probably responsible for the inhibition of neutrophil infiltration of the infected sites (Yang, Z., et al., *Science* 279(5353):1034-7 (1998)) and the absence of humoral immune response in Ebola virus infected patients. Baize, S., et al., *Nat Med*, 5(4):423-6 (1999). This protein may also act to over-activate many types of immune cells which can lead to massive intravascular apoptosis - essentially a shut-down of the immune system. Baize, S., et al., *Nat Med*, 5(4):423-6 (1999). The importance of the sGP to the Ebola virus life-cycle is also suggested by the fact it is present in all Ebola virus strains examined to date. Feldmann, H., et al., *Arch Virol Suppl*, 15:159-69 (1999).

The membrane glycoproteins are responsible for the attachment and penetration of the virions into target cells by mediating receptor binding and viral-cellular membrane fusion. Wool-Lewis, et al., *J. Virol*, 72(4):3155-60

(1998), Ito H., et al., *J. Virol*, 73(10):8907-12 (1999). They are synthesized as a single peptide precursor and cleaved by cellular enzymes (furin or cathepsin B) into the two mature forms, GP1 and GP2. The two GPs remain associated through a disulfide bond linkage and remain anchored in the viral membrane by a transmembrane (TM) domain. Ito H., et al., *J. Virol*, 73(10):8907-12 (1999); Malashkevich, V.N., et al., *Proc Natl Acad Sci U.S.A.*, 96(6):2662-7 (1999). The proteolytic cleavage site is composed of 4-5 basic amino acid residues that are similar to those found in the GPs of retrovirus, influenza, and paramyxoviruses. Garten, W., et al., *Biochimie*, 76(3-4):217-25 (1994). The cleavage event is essential for viral infectivity and is likely carried out by the same enzymes that cleave GPs of retrovirus or influenza viruses. Garten, W., et al., *Biochimie*, 76(3-4):217-25 (1994); Volchkov, V.E., et al., *Virology*, 245(1):110-9 (1994). In addition, Ebola virus GP may share a common mechanism of mediating viral infection with retroviral and influenza glycoproteins. Weissenhorn, W., et al., *Mol Membr Biol*, 16(1):3-9 (1999). Because membrane-bound GPs play critical roles in initiating virus infection and are also the predominant proteins exposed on the surface of the virions, they are the primary targets for neutralizing antibodies against the virus.

One of the properties of Ebola viruses that make them lethal to the host is their ability to suppress the host immune system. Serologic analysis of patients who died of the Ebola virus infection showed no signs of humoral or cellular immune responses. Baize, S., et al., *Nat Med,* 5(4):423-6 (1999). In contrast, antibodies against viral proteins and virus-specific T-cell activities were detected in a few survivors. Baize, S., et al., *Nat Med,* 5(4):423-6 (1999). Although the immunosuppressive mechanisms are yet to be understood, it is probable that the high levels of sGP and the immunosuppressive peptide in the GP are to blame for the absence of humoral and cellular immune responses in Ebola virus-infected patients.

The proteins that are responsible for the initial inflection of Ebola virus are the viral glycoproteins. Therefore, they are the target for neutralizing antibodies. However, Ebola virus has evolved "tricks" to prevent or delay the host immune response until it is too late to recover from the infection. Conventional approaches in producing vaccines against Ebola virus are likely to be ineffective for the following reasons: (1) viral glycoproteins produced in bacteria, yeast or insect cells are not properly glycosylated and therefore do

not have the true antigenicity of the viral proteins; (2) Ebola virus is too dangerous to be produced in large amounts as an inactivated-virus vaccine; and (3) procedures of inactivating the virus often destroy the conformation of the proteins, and therefore alter their antigenicity.

A preferred embodiment of the present invention is a recombinant viral vaccine having nucleic acids encoding one or more antigens of Ebola virus. Restriction maps and full sequence information of the Ebola virus, including the Zaire strain, is available through GenBank.

The genetic vaccine is a recombinant benign virus which is replication defective or incompetent and therefore is incapable of spreading beyond initially infected cells. For example, a recombinant adenoviral vaccine of the present invention mediates high levels of Ebola viral antigen expression for a period of two or more weeks, even though Ebola viral proteins have no functional relevance to recombinant virus function.

In another embodiment of the invention, the recombinant virus expresses one or more modified Ebola virus antigens. The modified Ebola virus antigens are preferably Ebola virus envelope glycoproteins and/or immunogically active parts thereof. Preferably the glycoproteins are modified GP and sGP glycoproteins. The Ebola virus GP and sGP glycoproteins are modified to destroy their pathogenic and immunosuppressive functions, but retain most of their natural antigenicity, since they are expressed, folded, glycosylated, and targeted to the cellular membrane inside the cells that can be productively infected by the Ebola virus. The modifications are carried out using standard molecular genetic manipulation techniques such as restriction digests and polymerase chain reaction.

A preferred modification of the Ebola virus envelope glycoprotein destroys the infective function of the Ebola virus GP. Any modification that destroys the infective function of Ebola virus can be used, but preferably the modification is a five amino acid deletion in the cleavage site of the GP. *See* Example 1. This cleavage site is composed of five basic amino acid residues, RRTRR, at position 501 from the start of the open reading frame. This deletion may be introduced into the Ebola virus GP cDNA using PCR amplification, which is performed by methods well known in the art.

Another preferred modification of the Ebola virus viral genome prevents synthesis of the sGP. Any modification that prevents synthesis may

be employed. Preferably the modification is directed to altering the RNA editing site from UUUUUUU to UUCUUCUU. *See* example 1.

Another preferred modification to Ebola virus antigen used in the present vaccines is immunosuppressive (IS) peptide located in GP2. The IS peptide motif is located at amino acids 585-609. A ten amino acid deletion between amino acide 590-600 removes its function. Second, each half of the IS peptide motif is reversed and duplicated. *See* **Figure 2**. This further ensures that its function has been destroyed and also increases its antigenicity.

Further it is readily apparent to those skilled in the art that variations or derivatives of the nucleotide sequences encoding Ebola virus antigen(s) of the present invention can be produced, which alter the amino acid sequence of the encoded protein. The altered expressed antigen(s) may have an altered amino acid sequence, yet still elicit immuneresponses that react with Ebola virus antigen(s), and are considered functional equivalents. In addition, fragments of the full-length genes that encode portions of the full-length protein may also be constructed. These fragments may encode a protein or peptide which elicits antibodies which react with Ebola virus antigen(s), and are considered functional equivalents.

Vaccination of an individual with the vaccines of the present invention results in entrance of adenoviral particles into cells and expression of Ebola virus antigen(s), such as the envelope glycoproteins, and the immune-stimulating cytokines. The expression of Ebola virus antigen(s) in cells induces strong and persistent immune responses as if an infection has occurred. The genetic vaccine has all of the immunogenicity of a natural infection, including expression of the natural viral proteins and long-lasting antigen stimulation, but does not have the pathogenicity of a true viral infection. In the vaccines of the present invention, the immunosuppressive mechanisms of Ebola virus are disabled, the antigens occur in their natural forms and are associated with the cell membrane, and immune stimulation lasts for weeks. The effects of this novel vaccine are long lasting and provide high rates of protection against Ebola virus infection.

The present invention is also directed to a method of immunizing a human against Ebola virus infection comprising administering the vaccines

described above. The techniques for administering these vaccines to humans are known to those skilled in the health fields.

By using the genetic vaccine of the present invention, individuals may be immunized against Ebola virus. Since the genetic vaccine can express high levels of antigens and/or a variety of glycoproteins simultaneously, the vaccinated individuals should be immunized against various strains Ebola virus. Additionally, since the genetic vaccine can express high levels of cytokines to mimic the body's response to natural viral infection, the body's immune response to such a geneticl vaccine against Ebola virus should be strong and long-lasting, thereby achieving a life-long immunity against the Ebola virus.

6. Formulation and Routes of Administration

The present invention also relates to a pharmaceutical composition comprising the vaccine(s) described above, and a pharmaceutically acceptable diluent, carrier, or excipient carrier. Additionally the vaccine may also contain an aqueous medium or a water containing suspension, often mixed with other constituents in order to increase the activity and/or the shelf life. These constituents may be salt, pH buffers, stabilizers (such as skimmed milk or casein hydrolysate), emulsifiers, and preservatives.

An adjuvant may be included in the pharmaceutical composition to augment the immune response to the viral antigen expressed from the recombinant virus. Examples of the adjuvant include, but are not limited to, muramyl dipeptide, aluminum hydroxide, saponin, polyanions, anamphipatic substances, bacillus Calmette-Guerin (BCG), endotoxin lipopolysaccharides, keyhole limpet hemocyanin (GKLH), interleukin-2 (IL-2), granulocyte-macrophage colony-stimulating factor (GM-CSF) and cytoxan, a chemotherapeutic agent which is believed to reduce tumor-induced suppression when given in low doses.

The present invention also provides kits for enhancing the immunity of a host to a pathogen. These kits may include any one ore more vaccines according to the present invention in combination with a composition for delivering the vaccine to a host and/or a device, such as a syringe, for delivering the vaccine to a host.

The vaccine according to the invention can be administered in a conventional active immunization scheme: single or repeated administration in a manner compatible with the dosage formulation, and in such amount as will be prophylactically effective, i.e. the amount of immunizing antigen or recombinant microorganism capable of expressing the antigen that will induce immunity in humans against challenge by the pathogenic virus or bacteria, such virulent Ebola virus, HIV, hepatitis A, B, C, D, and E virus, and bacillus tuberculous. Immunity is defined as the induction of a significant level of protection after vaccination compared to an unvaccinated human.

The vaccine of the present invention, i.e. the recombinant virus, may be administered to a host, preferably a human subject, via any pharmaceutically acceptable routes of administration. The routes of administration include, but are not limited to, intramuscular, intratracheal, subcutaneous, intranasal, intradermal, rectal, intramucusally, oral and parental route of administration. Routes of administration may be combined, if desired, or adjusted depending upon the type of the pathogenic virus to be immunized against and the desired body site of protection.

The route of administration can be particularly important in influencing the nature of induced immunity, and the degree of protection. For example, while parenteral administration may only activate a systemic immune response, whereas the oral route provides, in addition, mucosal immune response. The ability of the recombinant viruses of the present invention to elicit a mucosal immunity renders its application important in mucosally and sexually transmitted infection.

Doses or effective amounts of the recombinant virus may depend on factors such as the condition, the selected viral or bacterial antigen, the age, weight and health of the host, and may vary among hosts. In general, one skilled in the art understands that the amount of virus particles to be administered depends, for example, on the number of times the vaccine is administered and the level of response desired.

The appropriate titer of the recombinant virus of the present invention to be administered to an individual is the titer that can modulate an immune response against the viral or bacterial antigen and elicits antibodies against the pathogenic virus or bacteria from which the antigen is derived. An effective titer can be determined using an assay for determining the activity of

immunoeffector cells following administration of the vaccine to the individual or by monitoring the effectiveness of the therapy using well known *in vivo* diagnostic assays. For example, a prophylactically effective amount or dose of a recombinant adenovirus of the present invention may be in the range of from about 100 µl to about 10 ml of saline solution containing concentrations of from about $1x10^4$ to $1x10^8$ plaque forming units (pfu) virus/ml. When other plasmid DNA vectors are used, 1-1000 µg per administration is the preferred dose range. The dose may be the same for priming and boosting immunizations or it may be desired to alter quantity of recombinant viruses provided in the boosting phase as compared to the initial priming dose. The dose of an inoculum of the recombinant virus of the present invention is dictated by and dependent upon the unique characteristics of the particular recombinant virus and the particular immunologic effect to be achieved, as is well-recognized by the skilled artisan.

7. Methods of Enhancing the Immunity of a Host to Pathogens

The present invention also provides methods for enhancing the immunity of a host to pathogens with the recombinant viruses described above.

In one embodiment, the method is provided for enhancing the immunity of a host to a pathogenic virus. The method comprises: administering to the host a recombinant virus in an amount effective to induce an immune response. The recombinant virus comprises: an antigen sequence heterologous to the benign virus and encoding a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus; and an immuno-stimulator sequence heterologous to the benign virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen. The recombinant virus may preferably be replication-incompetent and not cause a malignancy naturally associated with the pathogenic virus in the host.

The recombinant virus may be administered to the host via any pharmaceutically acceptable route of administration. The recombinant virus may be administered to the host via a route of intramuscular, intratracheal,

subcutaneous, intranasal, intradermal, intramucosally, rectal, oral and parental administration.

In another embodiment, a method is provided for immunizing a host against a pathogenic virus with multiple antigens that elicit strong and long-lasting immune response to the multiple antigens. The method comprises: administering to the host a recombinant virus in an amount effective to induce an immune response. The recombinant virus comprises: a plurality of antigen sequences heterologous to the recombinant virus, each encoding a different viral antigen from one or more pathogenic viruses, expression of the plurality of the antigen sequences eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus. The recombinant virus may preferably be replication-incompetent and not cause malignancy that is naturally associated with the pathogenic virus(es) in the host.

Optionally, the recombinant virus may also comprise one or more immuno-stimulator sequences heterologous to the recombinant virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen.

In yet another embodiment, a method is provided for immunizing a host against a pathogenic virus by using multiple genetic vaccines or viruses. Multiple recombinant viruses may carry different antigens in each recombinant virus. The multiple recombinant viruses may be administered simultaneously or step-wise to the host.

The method comprises: administering to a host a first and second recombinant viruses in an amount effective to induce an immune response, wherein antibodies are produced. The first recombinant benign virus comprises: an antigen sequence heterologous to the first recombinant virus that encodes a viral antigen from a pathogenic virus, expression of the viral antigen eliciting an immune response directed against the viral antigen and cells expressing the viral antigen in the host upon infection of the host by the recombinant virus. The second recombinant virus comprises: an immuno-stimulator sequence heterologous to the second recombinant virus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the viral antigen. The first and second recombinant viruses

may preferably be replication-incompetent and not cause malignancy naturally associated with the pathogenic virus in the host.

According to the embodiment, the first and second recombinant virus may be any of a benign virus, such as replication-incompetent adenovirus, adeno-associated virus, SV40 virus, retrovirus, herpes simplex virus, Alpha virus, Venezuelan Equine Encephalitis (VEE) virus and vaccinia virus. Optionally, both the first and second recombinant viruses may be replication-incompetent adenovirus. Also optionally, one of the first and second recombinant viruses may be recombinant adenovirus and the other may be recombinant vaccinia virus.

In yet another embodiment, a method is provided for enhancing the immunity of a host to a pathogen. The method comprises: administering to the host a recombinant virus and one or more immuno-stimulators. The recombinant virus may be any of the recombinant viruses described above. In particular, the recombinant virus comprises one or more antigen sequences heterologous to the recombinant virus that encode one or more antigens from the pathogen. Expression of the antigen elicits an immune response directed against the antigen and cells expressing the antigen in the host upon infection of the host by the recombinant virus. The recombinant virus is preferably replication-incompetent and does not cause a malignancy naturally associated with the pathogen in the host. The pathogen may be a pathogenic virus such as HIV, hepatitis virus and Ebola virus, a pathogenic bacteria or parasite.

According to this embodiment, the immuno-stimulator may be any molecule that enhances the immunogenicity of the antigen expressed by the cell infected by the recombinant virus. Preferably, the immuno-stimulator is a cytokine, including, but not limited to interleukin-2, interleukin-8, interleukin-12, β- interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor, granulocyte-macrophage colony stimulating factor, and combinations thereof.

The cytokine may be administered into the host in a form of purified protein. Alternatively, the cytokine may be administered in a form of expression vector that expresses the coding sequence of the cytokine upon transfecting or transducing the cells of the host.

According to any of the above embodiments of the methods, the method may further comprise: administering to the host the recombinant virus

again to boost the immune response. Such a booster inoculation with the recombinant virus is preferably conducted several weeks to several months after the primary inoculation. To insure sustained high levels of protection against infection or an efficacious treatment of the disease(s) caused by infection of the pathogen, it may be helpful to re-administer the booster immunization to the host at regular intervals, for example, once every several years. The recombinant virus administered in the booster immunization may be the same as or different from the recombinant virus administered in the primary immunization.

Also according to any of the above embodiments of the methods, the method may further comprise: administering to the host a plasmid vector that encodes the same or different antigen(s) as that (or those) encoded by the recombinant virus. The plasmid vector is preferably a eukaryotic plasmid expression vector that expresses the antigen(s) upon transfection of the cells in the host.

Also according to any of the above embodiments of the methods, the method may further comprise: administering to the host a second recombinant virus to boost the immune response and/or to minimize neutralizing effects of the host's immune system on the recombinant viruses.

Optionally, the second recombinant virus comprises a second antigen sequence from a second pathogen that is different from the first antigen sequence comprised in the first recombinant virus administered in the primary immunization. Preferably, the second antigen sequence encodes the same type of antigen as that encoded by the first antigen sequence but from a different strain, serotype, or subtype/clade of the same pathogen. Alternatively, the second antigen may be a different type of antigen compared to the first antigen, for example, the first antigen being a surface protein and second antigen being a core protein of the same or different pathogen.

Also according to any of the above embodiments of the methods, the method may further comprise: administering to the host a viral vector prior to, concurrently, or post the administration of any of the above embodiment of the recombinant virus to minimize neutralizing effects of the host's immune system on the recombinant virus. Preferably, the viral vector is administered post the administration of the recombinant virus.

The viral vector may be the native progenitor of the recombinant virus. For example, the viral vector may be the wildtype adenovirus type 5 (Ad5) whereas the recombinant virus is a genetically modified Ad5.

Optionally, the viral vector may be the wildtype of or a genetically modified virus that is a different serotype of the recombinant virus. For example, the recombinant virus may be a genetically modified Ad5 whereas the viral vector is the wildtype of or a genetically modified adenoviral vector serotype other than Ad5, for example, serotype 1-4 or 6-51. It is noted that other serotypes discovered and/or classified later also fall within the scope of the invention.

For example, the recombinant virus is a recombinant Ad5 encoding one or more heterologous antigens and/or an immunostimulator while the viral vector may also be a recombinant adenovirus encoding the same or different antigens and/or the immunostimulator but of different serotype (e.g., Ad2, Ad4, Ad9, Ad12, Ad35 and Ad40). Such a serotype rotation is believed to enhance expression of the transgenes and increase immunogenicity of the vaccines. To verify this belief, a wildtype non-Ad5 vector can be administered to mice first and the levels of anti-adenovirus antibody are measured by ELISA 3 weeks after the injection. The recombinant Ad5 encoding a heterologous antigen (e.g., HBV core protein) is then administered to the mice 4-5 weeks after the primary injection. The levels of antibody against the heterologous antigen (e.g., the HBV core protein) can be measured 4-5 weeks after the secondary injection.

Also optionally, the viral vector may be a different virus from the recombinant virus. For example, the recombinant virus may be a genetically modified Ad5 whereas the viral vector is a genetically modified AAV, SV40 virus, retrovirus, herpes simplex virus, Alpha virus, Venezuelan Equine Encephalitis (VEE) virus or vaccinia virus. The viral vector may or may not comprise a heterologou antigen sequence. Preferably, the viral vector may comprise another antigen sequence which is the same or different from the antigen sequence carried by the recombinant virus.

Also optionally, the viral vector may be a chimeric vector modified based on the native progenitor of the recombinant virus. For example, if the native progenitor of the recombinant virus is adenovirus type 5, the viral vector may be a chimeric adenovirus type 5 with certain regions of the backbone

changed from type 5 to the corresponding regions from other adenovirus serotypes. This approach is believed to be advantageous because of the ease of cloning when only a portion of the backbone with the corresponding one of another serotype. This may be accomplished by constructing a shuttle vector by including Ad5 fiber DNA and switching the Ad5 fiber DNA partially or completely with that from another serotype of adenovirus. As shown in **Figure 62**, a right shuttle vector pR-Ad.5/35-6m is constructed to the replace the fiber region of Ad5 with that of Ad35. This right shuttle vector can be combined with a left shuttle vector and the Ad5 backbone to generate a chimeric Ad5 vector.

Up to date, 51 serotype of human adenovirus have been identified and divided into six subgroups from A to F. The adenovirus entry into the cells is a two- step process consisting of virus attachment to the membrane via the Ad fiber knob, followed by internalization upon binding of the penton base RGD motifs to $\alpha v\beta 3$ and $\alpha v\beta 5$ integrins on the cell surface. De Long et al. (1999) J. Clin. Microbiol. 37:3940; Sallusto et al. (1994) J. Exp. Med. 179:1109; Huang et al. (1995) J. Virol. 69:2257-2263; and Mathias et al. (1994) J. Virol. 68:6811-6814. The adenovirus fiber is considered to be a crucial mediator for high efficiency binding to target cells. Subgroup C, Ad5 fiber uses the coxsackievirus and adenovirus receptor (CAR) to mediate the high affinity binding. Nemerow (1999) Mol. Biol. Rev. 63:725-734. In CAR–deficient cells, Ad5 attachment occurs at much lower efficiency through alternative pathways involving interactions between the fiber and the MHC class I heavy chain $\alpha 2$ domain or between the penton and cellular integrins. Bergelson et al. (1997) Science 275:1320-1323.

The adenovirus fiber can be divided into three domains. The conserved N-terminal tail contains the sequences responsible for association with the penton base. De Long et al. (1999) J. Clin. Microbiol. 37:3940. The rod-like fiber shafts contains number of repeats ranging from 6 to 23 form the β sheets. Davison et al. (1999) J. Virol. 73:4513. The C-terminal contains globular knob domains, which both fiber shaft and knob are involved in the primary receptor interaction. Huang et al. (1996) J. Virol. 70:4502.

According to the present invention, for example, the fiber knob (i.e., the head), shaft, and/or penton base (i.e., the tail) in the backbone of adenovirus type 5 can be replaced by the corresponding region(s) of the

backbone from adenovirus serotype 1-4, and 6-51. **Figure 63** shows various embodiments of the chimeric vectors having the individual domains of the Ad5 fiber regions substituted with the corresponding domains of Ad35 fiber region. Preferably, the knob domain of the fiber region of Ad5 is swapped with the corresponding one from another serotype of adenovirus since the knob domain is believed to determine the receptor-ligand interaction.

For example, the recombinant virus is a recombinant Ad5 encoding one or more heterologous antigens and/or an immunostimulator while the chimeric viral vector may also be a recombinant Ad5 encoding the same or different antigens and/or the immunostimulator but having a fiber region from adenovirus of different serotype (e.g., Ad2, Ad4, Ad9, Ad12, Ad35 and Ad40). Such a serotype rotation is believed to enhance expression of the transgenes and increase immunogenicity of the vaccines. To verify this belief, an Ad5 vector carrying GFP can be administered to mice first and the levels of anti-GFP antibody are measured by ELISA 4 weeks after the injection. Another recombinant Ad5 also carrying GFP but having a fiber region from different serotype adenovirus (e.g, Ad9, Ad 11, or Ad35) is then administered to the mice 4-5 weeks after the primary injection. The levels of antibody against GFP can be measured 4-5 weeks after the secondary injection.

The methods described above may be used for prevention or treatment of diseases. In the method of treatment, the administration of the recombinant viruses of the present invention may be for either "prophylactic" or "therapeutic" purpose. When provided prophylactically, the recombinant virus is provided in advance of any symptom. The prophylactic administration of the recombinant virus serves to prevent or ameliorate any subsequent infection or disease. When provided therapeutically, the recombinant virus is provided at (or after) the onset of a symptom of infection or disease. Thus, the present invention may be provided either prior to the anticipated exposure to a disease-causing agent or after the initiation and/or progression of the infection or disease.

It is noted that the innovative approaches of the present invention may also be employed in the construction of cancer vaccines. For example, sequences encoding tumor-specific antigens may substitute the antigen sequence encoding viral antigen in any of the above embodiments of the recombinant virus and methods of using the same. Expression of tumor-

specific antigens in the host should elicit specific immune response for prevention in patients with an increased risk of cancer development (i.e., preventive immunization) or to enhance the treatment of cancer with other therapeutics, prevention of disease recurrence after primary surgery (anti-metastatic vaccination), or as a tool to expand the number of CTL in vivo, thus improving their effectiveness in eradication of diffuse tumors (treatment of established disease). In addition, the methods of the present invention may elicit an immune response in a patient that is enhanced ex vivo prior to being transferred back to the tumor bearer (i.e., the adoptive immunotherapy).

Also according to any of the above embodiments of the methods, the method may further comprise: harvesting serum from the host after the administration of the recombinant virus. The harvested serum should contain antibodies against the antigen(s) encoded by the recombinant virus. Optionally, the method may further comprise: isolating antibody or antibodies against the pathogen from the host after the administration of the recombinant virus. The harvested serum or isolated antibody can be stored for certain periods of time for further uses. For example, a healthy human volunteer can serve as the host and the serum or antibody collected from him/her may be administered back to him/herself or a different person later to in anticipation or in the event of infection of the pathogen as prophylactic or therapeutic agent by eliciting passive immunity against the pathogen. Optionally, the host may be a non-human animal and the serum harvested or antibody isolated from the animal immunized by the recombinant virus may be used as a prophylactic or therapeutic agent to treat a human or non-human animal in anticipation or in the event of infection of the pathogen such as in the outbreak of biological warfare.

It should be noted that modifications and changes can be made in the DNA sequence of any of the above-described antigens and immuno-stimulators included in the recombinant virus and still maintain functional equivalence of the mutant. For example, wildtype codons for the above-described antigens can be replaced with codons that are preferred by the host to be immunized, e.g., a human. Synthetic polynucleotide can be made to include the preferred codons for the "humanized" antigens. Such a humanization process may be advantageous in that by using the preferred codons, translation efficiency of the antigens expressed by the recombinant

virus can be significantly improved, which in turn can result in higher levels of humoral and/or cellular immune responses in the host. All of the above-described mutants fall within the scope of the present invention.

Standard procedures for endonuclease digestion, ligation and electrophoresis are carried out in accordance with the manufacturer's or supplier's instructions. Standard techniques are not described in detail and will be well understood by persons skilled in the art. Practicing the present invention employs, unless otherwise indicated, conventional methods of virology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See e.g. Sambrook, et al. *Molecular Cloning: A laboratory Manual*; *DNA Cloning: A Practical Approach*, vol I & II (D. Glover ed.); *Oligonucleotide Synthesis* (N. Giat, ed.); *Nucleic Acid Hybridization* (B. Hames & S. Higgins, eds., Current Edition); *Transcription and Translation* (B. Hames & S. Higgins, eds., Current Edition); *Fundamental Virology*, 2nd Edition, vol. I & II (B. N. Fields and D. M. Knipe, eds.)

The following examples are provided to illustrate the present invention without, however limiting the same thereto.

EXAMPLES

The following procedures are described to illustrate how to make a genetic vaccine of the present invention against various pathogenic viruses. The genetic vaccine is based on an adenoviral vector with modified antigens derived from the pathogenic virus (e.g., Ebola virus, Hepatitis B virus and HIV) inserted into the adenoviral backbone. Additionally, the recombinant adenovirus also carries multiple genes encoding various cytokines. The recombinant adenovirus is replication-incompetent but still retains adenoviral infectivity.

It is noted that genetic vaccine against other pathogenic viruses, bacteria and parasites may be constructed by one with ordinary skill in the art following similar procedures described in details below.

1. Genetic Vaccine against Ebola Virus

Embodiments of the genetic vaccine against Ebola virus and methods of their construction are described in detail as follows.

1) Genetic modification of the Ebola virus membrane glycoproteins

The modifications are carried out using standard molecular genetic manipulation techniques, such as restriction enzyme digests and polymerase chain reaction (PCR).

The glycoproteins of Ebola virus are modified to produce the optimal antigen for Ebola virus vaccine. Two modified forms of the GP proteins are constructed to have inactivated immunosuppressive and infectious mechanisms, but retain full natural antigenicity of the wild-type glycoproteins. The mRNA editing signal is deleted to prevent the production of the secreted glycoprotein (sGP), which is immunosuppressive; and (2) the proteolytic cleavage site of the glycoprotein precursor is deleted to prevent the formation of the functional glycoproteins (GP1 and GP2). Sanchez, A., et al., *Proc Natl Acad Sci U.S.A.* 93(8):3602-7 (1996). In one form the immunosuppressive peptide region is deleted to prevent its function, and in the other form, the immunosuppressive peptide motif is split in order to destroy its function, but

retain its immunogenicity. These steps produce effective and safe antigens for the vaccine.

The envelope glycoproteins (GP) of the Ebola virus are synthesized as a single precursor protein and cleaved into the two subunits (GP1 and GP2) by a cellular enzyme (furin) during transport. Volchkov, V.E., et al., *Proc Natl Acad Sci U.S.A.*, 95(10):5762-7 (1998). This proteolytic cleavage is essential for the formation of the mature glycoproteins and the release of the fusion peptide located at the C-Terminus of the cleavage site. The mature glycoproteins are incorporated into virions as trimers (each monomer is a heterodimer of GP1 and GP2 linked by a disulfide bond). Sanchez, A., et al., *J. Virol* 72(8):6442-7 (1998). The glycoproteins of Ebola virus are the major proteins exposed on the viral membrane surface, and are responsible for initiating virus entry into host cells. Therefore, they are a primary target for neutralizing antibodies.

The glycoprotein cleavage site is composed of five basic amino acid residues (RRTRR [SEQ ID NO: 10]) at position 501 from the start site of the open reading frame. The Ebola virus glycoprotein cleavage site is similar to the conserved sequences found in glycoproteins of other viruses, such as in the envelope protein of RSV or MuLV. We have previously shown that deletions or point mutations at these basic amino acid residues can block cleavage and render the glycoproteins non-functional in RSV. Dong, J.Y, et al., *J. Virol* 66(2):865-74 (1992).

To destroy the infective functions of the Ebola virus glycoprotein, the five basic amino acid residues in the cleavage site are deleted. This deletion is introduced into the Ebola virus GP cDNA using PCR amplification. Alternatively, the cleavage site can be altered, such as by site specific mutation resulting in elimination of cleavage.

Another important feature of the Ebola virus is that two forms of glycoproteins are synthesized from a single gene, a secreted from (sGP) and a membrane-bound form (GP). The two forms are generated as a result of an alternative RNA editing event at a sequence of seven uridines (at location 1020-1028 from the start site), which is highly conserved among all four Ebola virus subtypes. Sanchez, A., et al., *Proc Natl Acad Sci U.S.A.* 93(8):3602-7 (1996). The sGP is synthesized from un-edited mRNA and likely has immunosuppressive functions. The GP is synthesized from an edited mRNA

and likely has immunosuppressive functions. The GP is synthesized from an edited mRNA with insertion in one of the seven uridines. This RNA editing causes a frame-shift and results in a translation of the second reading frame that encodes the complete transmembrane glycoprotein (GP2).

To prevent the synthesis of sGP, the RNA editing site is modified from UUUUUUU [SEQ ID NO: 2] to UUCUUCUU [SEQ ID NO: 3] . In the cDNA, the equivalent sequence is AAAAAAA [SEQ ID NO: 4] and AAGAAGAA [SEQ ID NO: 5], respectively. This modification accomplishes two things: (1) all mRNAs encode only the GP (equivalent to the edited form with -1 frame shift); and (2) UUUUUU [SEQ ID NO: 6] encodes the same animo acid residues as UUCUUC [SEQ ID NO: 7], but prevents the possibility of further polymerase slipping at the stretch of the six uridines. The additional editing would cause deletion of one more uridine and further (-2) frame shifting. The mechanism of this modification is diagramed in **Figure 2**.

A third modification may be introduced into the Ebola virus glycoprotein relating to a deletion of the immunosuppressive (IS) peptide located in GP2. The IS peptide motif (amino acid 585-609, form the start site) is highly conserved in filoviruses and has a high degree of homologywith a motif in the glycoproteins of oncogenic retroviruses that has been shown to be immunosuppressive. Volchkov, V.E., et al., *FEBS Lett* 305(3):181-4 (1992); Will, C., et al., *J. Virol* 67(3):1203-10 (1993); Mitani, M., et al., *Proc Natl Acad Sci U.S.A.* 84(1):237-40 (1987); Gatot, J.S., et al., *J. Biol Chem* 273(21):12870-80 (1998); Denner, J., et al., *J Acquir Immune Defic Syndr Hum Retrovirol* 12(5):442-50 (1996). First, a ten amino acid deletion is introduced in the core region of the motif (between amino acid 590-600) to remove its function. Second, each half of the motif is reversed and duplicated to destroy function and increase antigenicity. It is believed that antibodies against the IS peptide may inhibit the immunosuppressive function of the Ebola viruses during an infection. The basic strategy of this modification is diagrammed in **Figures 3A-3C**.

As illustrated in **Figures 3A-3C**, modification of the immunosuppressive peptide (IS) is made on the GP2 gene. **Figure 3A** illustrates the wild type GP. **Figure 3B** illustrates GP with the 10 amino acid deletion of the IS peptide. **Figure 3C** illustrates the IS peptide, which is split, reversed and duplicated.

With these modifications, Ebola virus glycoproteins are generated that are non-functional, not immunosuppressive, yet they retain the natural antigenicity of GP. These modified GP sequences are used to generate antigens in the vaccines of the present invention against Ebola virus.

DNA sequences of the resulting altered GP genes are confirmed by sequence analysis. The modified GP sequences are then cloned intoplasmid vectors containing DNA elements necessary for efficient expression of these GPs in hostlan cells. Expression and correct localization to the cellular membrane is determined by transient transfections of HeLa or 293 cells and analyzed by Western blot and FACS, using polyclonal antibodies from hyperimmunized equine serum and anti-horse secondary antibodies labeled with horse radish peroxidase (HRP) or fluorescent tags, respectively.

2) Construction of a series of replication-defective adenoviral vaccines that mediate high levels of expression of the modified Ebola virus GPs

The vaccines of the present invention utilize a recombinant benign virus to carry modified antigens of Ebola virus to trick the host into mounting a robust immune defense against the Ebola virus. The preferred benign virus is a replication-defective adenovirus. These vectors are an excellent choice for vaccine expression, for several reasons. First, adenoviral vectors direct high levels of antigen expression that provides strong stimulation of the immune system. Second, the antigen that they express is processed and displayed in the transduced cells in a way that mimics pathogen-infected cells. This phase is believed to be very important in inducing cellular immunity against infected cells, and is completely lacking when conventional vaccination approaches are used. Third, adenoviral vectors infect dendritic cells which are very potent antigen-presenting cells. Diao, J. et al., *Gene Ther* 6(5):845-53 (1999); Zhong, L., et al., *Eur J Immunol* 29(3):964-72 (1999); Wan, Y., et al., *Int J Oncol* 14(4):771-6 (1999); Wan, Y., et al., *Hum Gene Ther* 8(11):1355-63 (1997). Fourth, these vectors can be engineered to carry immunoenhancing cytokine genes to further boost immunity. Fifth, adenoviruses naturally infect airway and gut epithelial cells in humans, and therefore the vaccine may be delivered through nasal spray or oral ingestion. And finally, the adenoviral vectors of this invention are safe because they are replication-defective

andhave been used in high doses (10^9 to 10^{12} i.p./dose) in clinical trials for gene therapy studies. Gahery-Segard, H., et al., *J. Clin Invest* 100(9):2218-26 (1997); Bellon, G.,et al., *Hum Gene Ther* 8(1):15-25 (1997); Boucher, R.C., et al., *Hum Gene Ther* 5(5):615-39 (1994). Indeed, even live viruses have been safely used in military recruits to prevent common colds.

This vector-construction system is also used to establish complex vectors that express multiple genes or regulatory mechanisms. For example, the vector construct is used to express multiple cytokines along with Ebola GP antigens in a single complex vector to further enhance the immune induction. Alternatively, antigens and cytokines are placed in separate vectors. This enables the manipulation of different combinations of cytokines and antigens by co-transduction (infection) with two or three vectors.

Construction of the adenoviral vectors is diagramed in **Figure 4**. The cDNA encoding a modified GP(s) is cloned into the left-end (E1 region) of the adenovirus genome using a shuttle vector pLAd (**Figure 4A** left side), resulting in a shuttle vector pLAd/EBO-GP. The pLAd/EBO-GP vector contains the left end of the adenoviral genome including the left long terminal repeats L-TR and the adenoviral packaging signal ψ. Genes encoding cytokines such as IL-2 and IL-4 are inserted into E4 region of the adenovirus vector using the shuttle vector pRAd (**Figure 4A,** right side), resulting in a shuttle vector pRAdIL2,4. The pRAdIL2,4 contains the right end of the adenoviral genome including the right long terminal repeats R-TR.

To construct an adenoviral vector carrying the GP gene only, the shuttle vector pLAd/EBO-GP is digested with appropriate restriction enzymes such as Xba I. The fragment containing the GP gene is ligated to an adenoviral backbone and pRAd vector.

To construct an adenoviral vector carrying both the GP gene in the E1 region and cytokine genes in the E4 region, both pLAd/EBO-GP and pRAdIL2, 4 are linearized and ligated to the backbone of the adenovirus (**Figure 4B**).

To generate recombinant adenoviral vectors, the ligated vector genome is transfected into 293 cells, in which only the correctly ligated genome with the two adenoviral terminal repeats can replicate and generate infectious viral particles. Human 293 cells (Graham et al., *J. Gen. Virol.*, 36: 59-72 (1977)), available from the ATCC under Accession No.: CRL1573), has adenovirus E1a and E1b genes stably integrated in its genome. The 293 cells

supplement the essential E1 gene of adenovirus that has been deleted from the vector backbone. The final vector has E1, E3 and partial E4 deleted and can only replicate in 293 cells, but not in target cells. The adenoviral vectors are amplified in 293 cells and purified by ultracentrifugation in cesium chloride gradients. Titers of vectors are determined by serial dilutions and counting of the infectious particle (ip) after infection of 293 cells.

3) Determination of immune respones to the genetic vaccine

An *in vitro* assay is used to quantitate the amount of neutralizing antibodies developed in response to the vaccine. The assay is based on a retroviral vector system which is based on a Moloney Murine Leukemia virus system. Vectors and packaging cells expressing GAG and POL proteins have been extensively characterized and are commercially available. A packaging vector construct that carries a β-galactosidase gene as a reporter is used. A novel vector construct expressing the membrane form of the Ebola virus GP is co-transfected with the β-Gal reporter vector resulting in a GAG-POL packaging cell line, which generates retroviral vector particles with the Ebola virus GP instead of its original envelope protein.

4) Determination of which modified GP antigen provides better production of neutralizing antibodies in animal models

The adenoviral vaccine vectors carrying the two GP variants are tested for their ability to induce an immune response to the Ebola virus GP in CD-1 mice (Charles River Laboratories; outbred stock of Swiss mice from Rockefeller Institute). Specifically, the neutralizing antibody titers and cytolytic T-lymphocyte (CTL) activities to the Ebola virus GP antigens induced by the GP variants with and without the IS motif are compared. Three groups of 30 8-week old mice are injected subcutaneously with 10^5 ip of adenoviral vectors expressing GP variant 1 (with IS peptide deleted), GP variant 2 (with IS peptide split and inverted) and β-Galactosidase (control vector), respectively. Six mice from each group are sacrificed (by CO_2 asphyxiation and cervical dislocation) at 1, 2, 4, 8 and 16 weeks post-vaccination, and their blood and

spleens are harvested. In addition, 6 mice are mock-vaccinated with saline and sacrificed 2 days later to provide preimmunization controls.

From mice injected with the control β-Gal vector, tissue sections from the sites of the vector injection are taken, fixed, and stained with the X-gal solution to determine the number and type of vector-transduced cells at various time-points post-infection. In addition, hemolysin staining isperformed to determine the degree of infiltration of various immune cells (neutrophils, macrophages, monocytes, etc.) at the site of the vector delivery.

Sera from vaccinated animals is assayed for total GP-binding antibodies using a standard 96-well plate ELISA protocol, as has been described. Van Ginkel, F.W., et al., *Hum Gene Ther* 6(7):895-903 (1995); Van Ginkel, F.W., et al., *J Immunol* 159(2):685-93 (1997). Neutralizing activity of the sera is analyzed by monitoring the infectious activity of the Ebola virus GP-pseudotyped retroviral vector (Wool-Lewis, et al., *J. Virol,* 72(4):3155-60 (1998)) on HeLa cells after the vector has been incubated with various serum concentrations. Expression of β-galactosidase in infected cell lysates serves as an indicator of the neutralizing activity of the serum (the lower the β-gal activity, the more EBO-β-Gal vectors have been neutralized) and is measured using a very sensitive fluorogenic substrate (Galacto-Light kit J) and a fluorescence plate reader. Anti-GP serum-neutralized infection rates are compared to infection rates in the absence of serum and in the presence of non-GP activated serum.

Cytotoxic lymphocytes (CTLs) are extracted from mouse spleen as previously described. Van Ginkel, F.W., et al., *Hum Gene Ther* 1995; 6(7):895-903; Dong, J.Y., et al., *Hum Gene Ther* 1996;7(3):319-31. They are mixed with a constant number of detached LnCaP cells (prostate carcinoma cells of epithelial origin) transduced with an adenoviral vector carrying an unmodified Ebola virus GP protein. Ratios of effector: target cells of 10:1, 3:1, and 1:1 are used. The cells are seeded into 96-well plates, and 24 hour later all unattached cells (which include all of the effector CTLs and dead or dying LnCaP cells) are removed, and the remaining viable (adherent) cells are quantitated by the MTT (3-(4,5-dimethylthiazol-20-yl) 2,5-diphenyl tetrazolium bromide) cleavage assay. This assay has been employed in detecting the lymphocyte cytotoxic activity (Ni, J., et al., *J Clin Lab Anal* 1996;10(1):42-52)

and compares favorably with the radioactive assays in terms of sensitivity, reliability and speed.

5) Immuno-enhancing functions of multiple cytokines and their effects on the efficacy of the genetic vaccines

To augment the effects of the vaccine, a vector-mediated gene transfer to express the immunoenhancing cytokines, such as IL2, IL4, IL12, INF-γ, and GM-CSF is used. Initially, each cytokine is separately cloned or the cytokines are cloned in various combinations into adenoviral vectors separate from the vectors encoding viral antigens. The immunoenhancing effects of individual cytokines or their combinations are studied by co-infecting with a vector encoding the cytokine and the vector carrying the antigens. The titers of serum antibodies are compared, as well as the time it takes to reach effective titers in animals inoculated with vaccines in combination with different cytokine-expressing vectors. These experiments allow the determination of whether immunoenhancing cytokines induce higher levels of antibodies, shorten the induction time, and prolong the immunity against the Ebola virus.

After determining the best-performing modified GP variant, the extent that the immune response elicited by it is enhanced by co-delivery to the immunization site of vectors carrying various cytokines is analyzed. Interleukin-2, either by itself or in combination with IL-4 or IL-12, has been demonstrated to strongly enhance the activation and proliferation of cytotoxic T-cells, natural killer (NK) cells and B-cells. Michael, B.N., et al., *Cell Immunol* 1994;158(1);105-15; Bruserud, O., et al.,*Eur J. Haematol* 1992;48(4);221-7; Jacobsen, S.E., et al., *Res Immunol* 1995;146(7-8):506-14; Wolf, S.F., et al., *Res Immunol* 1995;146(7-8);486-9; Tepper, R.I., *Res Immunol* 1993;144(8):633-7; O'Garra A., et al., *Res Immunol* 1993;144(8):620-5; Ohe, Y., et al., *Int J Cancer* 1993;53(3):432-7; Delespesse, G., et al., *Res Immunol* 1995;146(7-8):461-6. [36-43]. INF-γ stimulates the humoral immune response and increases the permeability of the blood vessel walls at the site of its secretion (Chensue, S.W., et al., *J Immunol* 154(11):5969-75 (1995); Szente, B.E., et al., *Biochem Biophys Res Commun* 203(3):1645-54 (1994); Adams, R.B., et al., *J. Immunol* 150(6):2356-63(1993)), while Gm-CSF

activates and attracts macrophages and other professional APCs to the site of the infection. Bober, L.A., et al., *Immunopharmacology* 29(2):111-9 (1995); Dale, D.C., et al., *Am J. Hematol* 57(1):7-15 (1998); Zhao, Y., et al., *Chung Hua I Hsueh Tsa Chih* 77(10): 32-6 (1997).

Six groups of 30 8-week old mice are injected subcutaneously with a mixture of $5x10^4$ ip of the selected GP variant vector and $5x10^4$ ip of one of the following vectors: Ad-β-Gal, Ad-IL2, Ad-IL2/IL4, Ad-IL2/IL12, Ad-IFN-γ and Ad-GM-CSF.

Six mice from each group are sacrificed and analyzed at 1, 2, 4, 8 and 16 weeks as described in Example 4. Analysis of total IgG is peformed using ELISA, neutralizing activity is assayed as interference with the ability of EBO-GP pseudotyped retroviral vector to infect HeLa cells, and anti-GP CTL activity is performed by mixing spleen-extracted CTLs with target LnCaP cells transduced with Ad-EBO-GP construct as described in Example 4. Levels of various cytokines in the serum are also quantitated by ELISA using available commercial assays. In some cases, these assays can distinguish between human and murine versions of the same cytokine, providing direct information on the expression levels of cytokines delivered using Adenovirus vectors and how they correlate with the development of the immune response.

After the individual cytokines are analyzed, those that performed best are tested in combinations. Four groups of 30 8-week old mice are injected subcutaneously with a mixture of $5x10^4$ i.p. of the selected GP variant vector and $5x10^4$ i.p. of up to 3 selected cytokine-expressing vectors (if fewer than 3 cytokine vectors are used, i.p. counts are made up with Ad-β-Gal vector). Six mice from each group are sacrificed at weeks 1, 2, 4, 8 and 16, and analyzed as described above.

To verify the robust and reproducible nature of the immune response to the GP vector and multiple cytokines in different species, the experiment as described above is reproduced in rabbits. Five groups of six white New Zealand rabbits are injected into the thigh muscle with one of the following vector combinations: the Ad-β-Gal vector (10^8 ip), the selected GP vector (2.5×10^5 ip plus $7.5x10^5$ ip of Ad-β-Gal), and three cytokine vector combinations ($2.5x10^5$ of each cytokine vector) plus the GP vector ($2.5x10^5$ ip), as described above. The animals are bled 2 days prior to vaccination (pre-immune bleed) and then according to the schedule described above. 5 to 10 ml of blood will

be extracted per session. Analysis is performed in a similar fashion to that of mice (see above).

Because genes coding for human cytokines are used in mouse and rabbit models, it is possible that their immune systems will have a non-identical (to human) response to those proteins. However, a high degree of homology exists between human and mouse cytokines and their receptors, and published reports on experiments using human or other hostian cytokines in mice indicate a high level of equivalency. If necessary, species-specific versions of these cytokines can be obtained and cloned into the adenoviral vectors of the present invention for species-targeted cytokine activity studies.

6) Optimizing the efficiency and rates of administration of the vaccine and conducting safety and pathogen challenge studies in non-primate and primate animal models

After determining the best combinations of the cytokines and antigens, the final version of the vaccine vectors are constructed. These complex recombinant adenoviral vectors deliver combinations of cytokines and antigens into target cells using a single vector. Dose-titer analysis in mice and rabbits are conducted to identify the lowest dose required to generate maximallevels of immune responses. Different routes of vaccine administration, such as intramuscular and intravenous injection, oral ingestion and nasal sprays are compared. For safety studies, dose escalation experiments in mice and rabbits are conducted until toxicity is observed or until levels ten times the effective dose have been reached. Finally, additional safety and pathogen challenge experiments are conducted in primates.

2. Genetic Vaccine Against HIV

Specific embodiments of the genetic vaccines against HIV and methods of their construction are described in detail as follows.

A. Construction of replication-defective adenoviral vaccines against HIV

1) Ad-E.T.R/IL2

An adenoviral vector, Ad-E.T.R/IL2, was constructed to carry coding sequences for multiple HIV antigens including Env, Tat, and Rev proteins, and interleukin-2 (IL-2) in the same vector. Expression of the HIV antigens and IL-2 is separately controlled by promoters located in different regions of the adenoviral vector. This design is believed to be able to ensure high level expression of both the viral antigens and the immuno-stimulator IL-2 and to enhance immunogenicity of the adenoviral vaccine. As shown by experimental data presented in the next section, this adenoviral vector is capable of eliciting strong humoral immune response in animals against HIV antigens.

The adenoviral vector, Ad-E.T.R/IL2, was constructed using strategies similar to those for constructing the adenoviral vaccines against Ebola virus as described in detail above. Briefly, EcoRI/XhoI restriction fragment from HIV-1 strain BH10 (HIV-1 or HTLV-IIIB, clade B, Accession No: M15654), which encodes wildtype envelope gp160 (full length gp 120 and gp41), full length wildtype Tat and full length wild type Rev, was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-E.T.R (**Figure 16A**). DNA sequence of this EcoRI/XhoI restriction fragment [SEQ ID NO: 14] is shown in **Figure 38**.

The sequence encoding IL-2 (with a silent mutation CTA to CTT at amino acid position 79 to delete the XbaI site) was inserted into E4 region of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pRAd-ORF6-IL2 (**Figure 16B**). DNA sequence encoding this mutated IL-2 (IL-2ΔX) [SEQ ID NO: 15] is shown in **Figure 39**.

Both pLAd-E.T.R and pRAd-OFR6-IL2 were linearized using appropriate restriction enzymes such as Xba I and EcoRI and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E.T.R/IL2.

2) Ad-3C/E^{m}ΔCΔT^{300}-G

Another adenoviral vector, Ad-3C/E^{m}ΔCΔT^{300}-G, was constructed to carry coding sequences for multiple HIV antigens including a modified Env (gp160) with deletion of the cleavage site between gp120 and gp41 and the cytosolic domain and Gag proteins, and three different cytokines (IL-2 with silent mutation CTA to CTT at amino acid position 79 to delete the XbaI site,

INF-γ, and GMCSF) in the same vector. Expression of the HIV antigens and the cytokines is separately controlled by promoters located in different regions of the adenoviral vector. This design is believed to be able to ensure high level expression of both the viral antigens and the immuno-stimulators and to enhance immunogenicity of the adenoviral vaccine. As shown by experimental data presented in the next section, this adenoviral vector is capable of eliciting strong humoral immune response in animals against HIV antigens.

The adenoviral vector, Ad-3C/$E^m\Delta C\Delta T^{300}$-G, was constructed using strategies similar to those for constructing the adenoviral vaccines against Ebola virus as described in detail above. Briefly, the sequence from HIV-1 strain BH10 that encodes Env/gp160 (nucleotide position 5580-7850) was modified to delete the sequences encoding the cleavage site (REKR [SEQ ID NO: 11] encoded by nucleotide at position 7101-7112) and the cytosolic domain of 100 amino acids in length (encoded by nucleotide at position 7850-8150), and then, along with the sequence encoding a full length Gag, inserted into the right end (E4 region) of the adenoviral genome using a shuttle vector. DNA sequence of this modified Env ($E^m\Delta C\Delta T$ (BH10) [SEQ ID NO: 16] and that of the full length Gag [SEQ ID NO: 17] (amino acid sequence of which is SEQ ID NO: 18, **Figure 41B**) are shown in **Figures 40** and **41A**, respectively.

These two HIV antigens are expressed separately from a CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at two splicing acceptor sites, SA_1, and SA_2. To facilitate efficient cloning of various gene fragments, a cloning vector SD/SA1.2.3 was constructed to include a retroviral SD site and multiple retroviral SA sites, SA_1, SA_2, SA_3 and SA_4. In this example, the SD and SA sites were derived from Moloney murine leukemia virus (MMLV) and their sequences are shown below:

SD site (MMLV nt 204-210): AGGTAAG [SEQ ID NO: 72]; and

SA_{1-4} site (MMLV nt 560-568): CTGCTGCAG [SEQ ID NO: 73].

Each of the SD site, and the SA_1, SA_2, SA_3 and SA_4 (SA_{1-4}) sites which share the same sequence was inserted into the multiple cloning site of a cloning vector pSP73 by using standard PCR mutagenesis. As illustrated in **Figure 37**, SA_1 was inserted immediately downstream from SD site, followed by SA_2, SA_3 and SA_4. To test the levels of expression of multiple genes via the SD/SA mechanism, the GFP (green fluorescence protein) gene was inserted between

SD/SA_1 and SA_2, SA_2 and SA_3, SA_3 and SA_4, and after SA_4. The ratio of expression levels in these four sites is 10:1:5:4.

DNA sequences encoding $E^m\Delta C\Delta T$ and Gag were inserted into the cloning vector SD/SA1.2.3 after SD/SA_1, and SA_2, respectively. The resulting vector was digested with EcoRV and XhoI and the fragment containing $E^m\Delta C\Delta T$ and Gag was inserted into an adenoviral shuttle vector, resulting in pRAd-ORF6-cmv- $E^m\Delta C\Delta T^{300}$-G (**Figure 17A**). Shuttle vectors capable of expressing other proteins (as shown below) via the retroviral SD/SA mechanism were constructed using the same strategy.

Sequences encoding multiple immuno-stimulators, including IL-2 (with a silent mutation caused by deletion of Xba I site), INF-γ, and GMCSF, were inserted into E1 region of the adenoviral genome using a shuttle vector. These three immuno-stimulators are expressed separately from another CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at three splicing acceptor sites, SA_1, SA_2, and SA_3. The shuttle vector produced is designated pLAd-3C (**Figure 17B**).

Both pRAd-ORF6-cmv- $E^m\Delta C\Delta T^{300}$-G and pLAd-3C were linearized using appropriate restriction enzymes such as Xba I and EcoRI and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-3C/$E^m\Delta C\Delta T^{300}$-G.

3) Ad-3C/$E^m\Delta C\Delta T^{99}$.T.R-G

Yet another adenoviral vector, Ad-3C/$E^m\Delta C\Delta T^{99}$.T.R-G, was constructed to carry coding sequences for multiple HIV antigens from strain pNL4-3 (Accession No: M19921) including a modified Env (gp160 with deletion of the cleavage site and the cytoplasmic domain of 33 amino acids in length), full length Rev and Gag proteins, and three different cytokines (IL-2 with silent mutation CTA to CTT at amino acid position 79 to delete the XbaI site, INF-γ, and GMCSF) in the same vector. Expression of the HIV antigens and the cytokines is separately controlled by promoters located in different regions of the adenoviral vector. This design is believed to be able to ensure high level expression of both the viral antigens and the immuno-stimulators and to enhance immunogenicity of the adenoviral vaccine. As shown by experimental data presented in the next section, this adenoviral vector is

capable of eliciting strong humoral immune response in animals against HIV antigens.

The adenoviral vector, Ad-3C/E$^{m}\Delta C\Delta T^{99}$.T.R-G, was constructed using strategies similar to those for constructing the adenoviral vaccines against Ebola virus as described in detail above. Briefly, the sequence from HIV-1 strain pNL4-3 that encodes Env/gp160 (nucleotide position 6221-8688) was modified to delete the sequences encoding the cleavage site (encoded by nucleotide at position 7736-7747) and the cytosolic domain (encoded by nucleotide at position 8687-8785) in length, and then, along with sequences encoding full length Tat, Rev, and Gag (from HIV strain BH10), inserted into the right end (E4 region) of the adenoviral genome using a shuttle vector.

These three HIV antigens are expressed separately from a CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at three splicing acceptor sites, SA, SA_2, and SA_3. The shuttle vector produced is designated pRAd-E$^{m}\Delta C\Delta T^{99}$.T.R-G (**Figure 18**). DNA sequence encoding the modified Env, and full length Tat and Rev [SEQ ID NO: 19] is shown in **Figure 42**. DNA and amino acid sequences of the full length Gag from HIV strain BH10 [SEQ ID NO: 17] are shown in **Figures 41A** and **41B**, respectively.

The shuttle vectors, pRAd-E$^{m}\Delta C\Delta T^{99}$.T.R.-G and pLAd-3C (**Figure 17B**) were linearized using appropriate restriction enzymes such as Xba I and EcoRI and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-3C/E$^{m}\Delta C\Delta T^{99}$.T.R.-G.

4) Ad-E$^{m}\Delta V_{1,2}$ ΔC ΔT^{99}.T.R-IL2/G.IL2

Yet another adenoviral vector, Ad-E$^{m}\Delta V_{1,2}$ ΔC ΔT^{99}.T.R/G.IL2, was constructed to carry coding sequences for multiple HIV antigens from HIV-1 strain pNL4-3. The sequence from HIV-1 strain pNL4-3 that encodes Env/gp160 (nucleotide position 6221-8686) was modified to delete the sequences encoding the V1 and V2 loops at position 6602-6796 nt and insert nucleotide sequence GGA GCT GGT [SEQ ID NO: 12] that encodes amino acid sequence GAG [SEQ ID NO: 13]. This HIV Env/gp160 was also modified to delete the cleavage site encoded by nucleotide at position 7736-7747 (ΔC) and the 33-aa cytosolic domain encoded by nucleotide at position 8687-8785

(ΔT^{99}). Along with the sequences encoding full length Rev (R) and Tat (T), the modified *env* was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector. DNA sequence encoding the insert ($E^m\Delta V_{1,2}$ ΔC ΔT.T.R) [SEQ ID NO: 20] is shown in **Figure 43**.

Additionally, IL-2 (with a silent mutation caused by deletion of Xba I site, DNA SEQ ID NO: 15) was inserted downstream from the modified *env*. Both the modified Env and IL-2 are expressed separately from a CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at two splicing acceptor sites, SA_1 and SA_2/SA_3. The shuttle vector produced is designated pLAd- $E^m\Delta V_{1,2}$ ΔC ΔT.T.R-IL2 (**Figure 19A**).

Sequences encoding IL-2 (with a silent mutation caused by deletion of Xba I site, DNA SEQ ID NO: 15) and Gag from HIV-1 strain BH10 (nt 112-1650, DNA SEQ ID NO: 17) were inserted into E4 region of the adenoviral genome using a shuttle vector. These two proteins are expressed separately from a CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at two splicing acceptor sites, SA_1 and SA_2. The shuttle vector produced is designated pRAd-ORF6-G.IL2 (**Figure 19B**).

Both pLAd-cmv- $E^m\Delta V_{1,2}$ ΔC ΔT.T.R-G and pRAd-ORF6-G.IL2 were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-$E^m\Delta V_{1,2}$ ΔC ΔT.T.R-G/G.IL2.

5) Ad-E^mΔC.T.R.N/G.IL2

Yet another adenoviral vector, Ad-E^mΔC.T.R.N/G.IL2, was constructed to carry coding sequences for multiple HIV antigens from HIV-1 strain BH10. The sequence from HIV-1 strain BH10 that encodes full length Env/gp160 (nucleotide position 5580-8150), Tat, Rev, and Nef was modified by deleting the sequence encoding the cleavage site of Env and inserting a SpeI restriction site. DNA sequence of this insert [SEQ ID NO: 21] is shown in **Figure 44**, and was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-E^mΔC.T.R.N (**Figure 20**).

Both pLAd-E^mΔC.T.R.N and pRAd-ORF6-G.IL2 (**Figure 19B**) were linearized using appropriate restriction enzymes and ligated to the backbone

of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔC.T.R.N/G.IL2.

6) Ad-E^{m}ΔC.N /G.IL2

Yet another adenoviral vector, Ad-E^{m}ΔC.N/G.IL2, was constructed to carry coding sequences for multiple HIV antigens from HIV-1 strain BH10. The sequence from HIV-1 strain BH10 that encodes full length Env/gp160 (nucleotide position 5580-8150, with preceding Kozak sequence), Tat, Rev, and Nef was modified by deleting the sequences encoding the cleavage site of Env, Tat and Rev, and inserting a SpeI restriction site. DNA sequence of this insert [SEQ ID NO: 22] is shown in **Figure 45**, and was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-E^{m}ΔC.N (**Figure 21**).

Both pLAd-E^{m}ΔC.N and pRAd-ORF6-G.IL2 (**Figure 19B**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔC.N/G.IL2.

7) Ad-E^{m}ΔCΔT^{300}.T /G.IL2

Yet another adenoviral vector, Ad-E^{m}ΔC ΔT^{300}.T/G.IL2, was constructed to carry coding sequences for multiple HIV antigens from HIV-1 strain BH10. The sequence from HIV-1 strain BH10 that encodes full length Env/gp160 (nucleotide position 5580-8150) was modified by deleting the sequence encoding the cleavage site and a 300 nt sequence encoding the cytosolic domain, but still including sequence for full length Tat (T). DNA sequence of this insert [SEQ ID NO: 23] is shown in **Figure 46**, and was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-E^{m}ΔC ΔT^{300}.T (**Figure 22**).

Both pLAd-E^{m}ΔC ΔT^{300}.T and pRAd-ORF6-G.IL2 (**Figure 19B**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔC ΔT^{300}.T/G.IL2.

8) Ad-E^{m}ΔC/ E^{m}ΔC

Yet another adenoviral vector, Ad-$E^m\Delta C$/ $E^m\Delta C$, was constructed to carry coding sequences for two copies of a modified Env from HIV-1 strain BH10. The sequence from HIV-1 strain BH10 that encodes full length Env/gp160 (nucleotide position 5580-8150, preceding Kozak sequence) was modified by deleting the sequence encoding the cleavage site. DNA sequence of the modified Env [SEQ ID NO: 24] is shown in **Figure 47**, and was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-$E^m\Delta C$ (**Figure 23A**).

The DNA sequence encoding the modified Env ($E^m\Delta C$) [SEQ ID NO: 24] was also inserted into E4 region of the adenoviral genome using a shuttle vector, resulting in shuttle vector pRAd-ORF6-$E^m\Delta C$ (**Figure 23B**).

Both pLAd-$E^m\Delta C$ and pRAd-ORF6-$E^m\Delta C$ were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-$E^m\Delta C$/ $E^m\Delta C$.

9) Ad-E^m.V3^m/G.IL-2

Yet another adenoviral vector, Ad-E^m.V3^m/G.IL-2, was constructed to carry coding sequences for modified HIV-1 Env having multi-clade V3 loops and Gag, and IL-2. Sequences encoding V3 loop from clade B, A, C, D, E, F, and G within Group M of HIV-1 are shown in **Figure 48**. As shown in **Figure 48**, for clade B (HIV-1 strain BH10) DNA sequence encoding V3 loop, nt 885-992 [SEQ ID NO: 25], was chosen. In this particular embodiment, for clade A (HIV-1 strain 192UG037WHO.01083hED) DNA sequence encoding V3 loop, nt 888-992 [SEQ ID NO: 26], was chosen. For clade C (HIV-1 strain 192BR025WHO.01093hED) DNA sequence encoding V3 loop, nt 876-980 [SEQ ID NO: 27], was chosen. For clade D (HIV-1 strain 192UG024.2) DNA sequence encoding V3 loop, nt 888-989 [SEQ ID NO: 28], was chosen. For clade E (HIV-1 strain 193TH976.17) DNA sequence encoding V3 loop, nt 894-998 [SEQ ID NO: 29], was chosen. For clade F (HIV-1 strain 193BR020.17) DNA sequence encoding V3 loop, nt 888-992 [SEQ ID NO: 30], was chosen. For clade G (HIV-1 strain 192RU131.9) DNA sequence encoding V3 loop, nt 885-989 [SEQ ID NO: 31], was chosen.

The DNA sequences encoding V3 loops from HIV clade A, C, D, E, F, and G were ligated by PCR to form a single fragment containing multiclade V3

loops. Primers for cloning these V3 loops from their cognate HIV clades are listed in **Figure 57**. Since V3 loop of HIV clade B is already contained in the backbone of HIV-1 gp120, the cloned V3 loops from clade A, C, D, E, F, and G were inserted after V3 loop of clade B.

Figure 24 illustrate a process for generating the ligated multiclade V3 loops by PCR and subsequent cloning into a construct encoding a modified gp120 of clade B. As illustrated in **Figure 24**, each of the gene fragments encoding the envelope V3 loop region from clade A, C, D, E, F, and G was individually amplified by PCR using a set of forward and reverse primers listed in **Figure 57**. Parameters for the PCR cycles are the following:

denature: 94 °C for 1 min;
annealing: 50 to 60 °C for 30 sec; and
extension: 72 °C for 1 min;
for 20 cycles.

The PCR product encoding V3 loop of one clade was ligated with another using PCR. For example, the PCR products encoding V3 loops of clade A and C were mixed together, ligated and amplified by PCR using the primers 1 and 4 as shown in **Figure 24**, procuding an A/C fragment. Similarly, a PCR product encoding the ligated V3 loops of clade D and E was generated using primers 5 and 8, producing a D/E fragment; and clade F and G using primers 9 and 12 (**Figure 24**), producing a F/G fragment.

Still refering to **Figure 24**, the A/C and D/E fragments were ligated by PCR using primers 1 and 8 and cloned into a vector at EcoRI and BamHI sites. The F/G fragment was restriction digested with BamH1 and Xbal and fused with the sequence A/C/D/E to generate the multi-clade sequence ACDEFG ($V3^m$).

To generate two repeats of the multi-clade ACDEFG sequence, the final PCR product encoding the multi-clade ACDEFG sequence was restriction digested with Aval (at primer 1 and 12) and re-ligated head-to-tail, yielding the two repeat multiclade sequence 2x $V3^m$. The DNA sequence encoding $V3^m$ or 2x $V3^m$ was then inserted after the sequence encoding V3 loop of clade B in a construct encoding gp120 which was modified as follows.

DNA sequence encoding Env (nt 5580-8150) from HIV strain BH10 (clade B) was modified by a) deleting the sequence encoding the cleavage site (nt 7101-7112); b) deleting V1 and V2 loops (nt 5961-6161) and inserting

nucleotide sequence GGA GCT GGT [SEQ ID NO: 12] that encodes amino acid sequence GAG [SEQ ID NO: 13]; c) inserting the multi-clade V3 loop ($V3^m$) sequence at position nt 6572; and d) replacing gp41 transmembrane domain sequence with a GPI anchor sequence encoding glycophosphatidyl inositol, SWLLLLLLSLSLLQATDFMSL [SEQ ID NO: 9]. DNA sequence encoding this modified Env [SEQ ID NO: 32] (the amino acid sequence of which is SEQ ID NO: 33, **Figure 49B**) is shown in **Figure 49A**, and was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-E^m.$V3^m$ (**Figure 25**).

Both pLAd-E^m.$V3^m$ and pRAd-ORF6-G.IL2 (**Figure 19B**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^m.$V3^m$/G.IL2.

10) Shuttle Vector pLAd-E^m.2x$V3^m$

To increase the expression level of the multi-clade V3 loops, the sequnece encoding two repeats of $V3^m$ sequence (2x$V3^m$, constructed above) was inserted into the sequence encoding the modified Env described in section 9) above. The resulting shuttle vector is designated pLAd-E^m.2x$V3^m$ and is shown in **Figure 26**.

11) Shuttle Vectors encoding p17 and/or p24

In nature the Pr55 Gag protein can be processed into four different proteins, p17MA, p24CA, p7NC, and p6. The p17MA protein remains associated with the inner side of the lipid envelope, and plays an important role in anchoring of envelope to the viral particle. The p24CA protein of all retroviruses contains a major homology region (MHR) that is required for efficient viral replication and particle production. Elispot data obtained implicates that p17MA (or p17) and p24CA (or p24) may have contributed significantly the specific CTL response in the Pr55 gag protein in peptide mapping experiments. According to the present invention, these HIV structural proteins are expressed by the recombinant virus to elicit specific CTL response to HIV infection. Further, these structure proteins can be modified to include a signal peptide (e.g., the HIV gp120 signal peptide encoded by SEQ ID NO: 74:

atgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatggggcaccatgctccttggga tgttgatgatctgtagtgct) sequence which facilitates the secretion of these intracellular proteins by the infected cells. Moreover, by adding a membrane anchoring domain (e.g, the HIV gp41 transmembrane domain encoded by SEQ ID NO: 75:

ttattcataatgatagtaggaggcttggtaggtttaagaatagtttttgctgtactttctgtagtgaatagagttagg cagggatattcaccattatcgtttcagacccacctcccaatcccgagggga) to the secreted form of the HIV protein, such a modified HIV structural protein is rendered membrane bound, which better presents the HIV antigen to the body's immune system. These modifications may confer a much stronger immunogenicity to the mutant antigen than the native antigen which are trapped intracellularly.

Adenoviral shuttle vectors were constructed to encode the processed Gag proteins, p17, p24, and p17/24, each in three different forms: natural form, secreted form and membrane bound form.

DNA sequences of p17/p24 in the three forms [SEQ ID NOs: 34-36] are shown in **Figure 50A** (corresponding amino acid sequences [SEQ ID NOs: 37-39], **Figure 50B**) and were each inserted into E4 region of the adenoviral genome using a shuttle vector, resulting in shuttle vector pRAd-ORF6-p17/24 (natural form, **Figure 27A**), pRAd-ORF6-p17/24sec (secreted form, **Figure 27B**), and pRAd-ORF6-p17/24MB (membrane-bound form, **Figure 27C**), respectively.

DNA sequences of p17 in the three forms [SEQ ID NOs: 40-42] are shown in **Figure 51A** (corresponding amino acid sequences [SEQ ID NOs: 43-45], **Figure 51B**) and were each inserted into E4 region of the adenoviral genome using a shuttle vector, resulting in shuttle vector pRAd-ORF6-p17 (natural form, **Figure 28A**), pRAd-ORF6-p17sec (secreted form, **Figure 28B**), and pRAd-ORF6-p17MB (membrane-bound form, **Figure 28C**), respectively.

DNA sequences of p24 in the three forms [SEQ ID NOs: 46-48] are shown in **Figure 52A** (corresponding amino acid sequences [SEQ ID NOs: 49-51], **Figure 52B**) and were each inserted into E4 region of the adenoviral genome using a shuttle vector, resulting in shuttle vector pRAd-ORF6-p24 (natural form, **Figure 29A**), pRAd-ORF6-p24sec (secreted form, **Figure 29B**), and pRAd-ORF6-p24MB (membrane-bound form, **Figure 29C**), respectively.

The pLAd- and pRAd-shuttle vectors constructed above can be combined in a combinatorial way to generate a wide variety of recombinant adenoviral vectors. The following are just a few examples of such recombinant adenoviral vectors.

12) Ad-E^{m}.2xV3^{m}/p17/24MB

Figures 30A-B illustrate the construction of a recombinant adenoviral vector encoding modified Env containing two copies of multi-clade V3 loops and p17/p24 in membrane-bound form. As illustrated in **Figures 30A-B**, pLAd-E^{m}.2xV3^{m} (details of the vector shown in **Figure 26**) and pRAd-ORF6-p17/24MB (details of the vector shown in **Figure 27C**) were linearized using EcoR1 and Xba1 restriction enzymes and ligated to the backbone of the adenovirus, resulting in the recombinant adenoviral vector Ad-E^{m}.2xV3^{m}/p17/24MB.

13) Ad-E^{m}.2xV3^{m}/p17MB

Figures 31A-B illustrate the construction of a recombinant adenoviral vector encoding modified Env containing two copies of multi-clade V3 loops and p17 in membrane-bound form. As illustrated in **Figures 31A-B**, pLAd-E^{m}.2xV3^{m} (details of the vector shown in **Figure 26**) and pRAd-ORF6-p17MB (details of the vector shown in **Figure 28C**) were linearized using EcoR1 and Xba1 restriction enzymes and ligated to the backbone of the adenovirus, resulting in the recombinant adenoviral vector Ad-E^{m}.2xV3^{m}/p17MB.

14) Ad-E^{m}.2xV3^{m}/p24MB

Figures 32A-B illustrate the construction of a recombinant adenoviral vector encoding modified Env containing two copies of multi-clade V3 loops and p24 in membrane-bound form. As illustrated in **Figures 32A-B**, pLAd-E^{m}.2xV3^{m} (details of the vector shown in **Figure 26**) and pRAd-ORF6-p24MB (details of the vector shown in **Figure 29C**) were linearized using EcoR1 and Xba1 restriction enzymes and ligated to the backbone of the adenovirus, resulting in the recombinant adenoviral vector Ad-E^{m}.2xV3^{m}/p24MB.

15) Ad-E^{m}.ΔCΔT^{300}.2xV3^{m}.T./p17/24sec

DNA sequence encoding Env (including Tat1 (nt 5189-5403) and Tat2 (7734-7779)) from HIV strain BH10 was modified by a) deleting the sequence encoding the cleavage site (nt 7101-7112); b) deleting V1 and V2 loops (nt 5961-6161) and inserting nucleotide sequence GGA GCT GGT [SEQ ID NO: 12] that encodes amino acid sequence GAG [SEQ ID NO: 13]; c) inserting two copies of the multi-clade V3 loop (2xV3^{m}) sequence at position nt 6572; and d) deleting the cytosolic domain of 100 amino acids in length (encoded by nucleotide at position 7850-8150). DNA sequence encoding this modified Env [SEQ ID NO: 52] (the amino acid sequence of which is SEQ ID NO: 53, **Figure 53B**) is shown in **Figure 53A**, and was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-E^{m}ΔCΔT^{300}.2xV3^{m}.T (**Figure 33**).

Both pLAd-E^{m}ΔCΔT^{300}.2xV3^{m}.T and pRAd-ORF6-p17/24sec (**Figure 27B**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔCΔT^{300}.2xV3^{m}.T./p17/24sec.

16) Ad-E^{m}ΔCΔT^{300}.2xV3^{m}.T./p17/24MB

Both pLAd-E^{m}ΔCΔT^{300}.2xV3^{m}.T (**Figure 33**) and pRAd-ORF6-p17/24MB (**Figure 27C**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔCΔT^{300}.2xV3^{m}.T./p17/24MB.

17) Ad-E^{m}ΔCΔT^{99}.2xV3^{m}.T.R/p17/24sec

DNA sequence encoding Env (including Tat1 (nt 5189-5403), Rev1 (nt 5328-5403), Tat2 (7734-7779) and Rev2 (7734-8008)) from HIV strain BH10 was modified by a) deleting the sequence encoding the cleavage site (nt 7101-7112); b) deleting V1 and V2 loops (nt 5961-6161) and inserting nucleotide sequence GGA GCT GGT [SEQ ID NO: 12] that encodes amino acid sequence GAG [SEQ ID NO: 13]; c) inserting two copies of the multi-clade V3 loop (2xV3^{m}) sequence at position nt 6572; and d) deleting the cytosolic domain of 33 amino acids in length (nt 8687-8785). DNA sequence encoding this modified Env [SEQ ID NO: 54] (the amino acid sequence of which is SEQ ID NO: 55, **Figure 54B**) is shown in **Figure 54A**, and was

inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector, resulting in a shuttle vector pLAd-E^{m}ΔCΔT^{300}.2xV3^{m}.T.R (**Figure 34**).

Both pLAd-E^{m}ΔCΔT^{300}.2xV3^{m}.T.R and pRAd-ORF6-p17/24sec (**Figure 27B**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔCΔT^{99}.2xV3^{m}.T.R/p17/24sec.

18) Ad-E^{m}ΔCΔT^{99}.2xV3^{m}.T.R/p17/24MB

Both pLAd-E^{m}ΔCΔT^{99}.2xV3^{m}.T.R (**Figure 34**) and pRAd-ORF6-p17/24MB (**Figure 27C**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔCΔT^{99}.2xV3^{m}.T.R/p17/24MB.

19) Ad-E^{m}ΔCΔT^{300}.2xV3^{m}.T/G.PI

Peptide mapping and Elispot data indicate that specific regions of the Gag protein may play significant roles in eliciting CTL response in animals immunized with the adenoviral vectors of the present invention. To facilitate efficient expression of p17MA and p24CA by the adenoviral vector, DNA sequence encoding the protease (PI, DNA SEQ ID NO: 56, **Figure 55A;** amino acid SEQ ID NO: 57, **Figure 55B**) from the *pol* region of HIV strain BH10 was inserted into a region downstream from the sequence encoding Gag in a shuttle vector pRAd-ORF6-G.PI (**Figure 35**). As illustrated in **Figure 35**, Gag and PI are expressed separately from a CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at two splicing acceptor sites, SA_1 and SA_2/ SA_3.

Both pLAd-E^{m}ΔCΔT^{300}.2xV3^{m}.T (**Figure 33**) and pRAd-ORF6/G.PI (**Figure 35**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-E^{m}ΔCΔT^{300}.2xV3^{m}.T/G.PI.

20) Ad-E^{m}ΔCΔT^{300}.2xV3^{m}.T/G-PI

Alternatively, the HIV protease PI was expressed as a fusion protein with Gag by inserting a C residue at position nt1410 to allow *pol* to be read within the same reading frame of *gag*. DNA [SEQ ID NO: 58] and amino acid

[SEQ ID NO: 59] sequences of the Gag-PI fusion protein are shown in **Figures 56A** and **56B,** respectively. As illustrated in **Figure 36**, Gag and PI are expressed from the same CMV promoter within the same reading frame. The resulting shuttle vector is designated as pRAd-ORF6/G-PI.

Both pLAd-$E^{m}\Delta C\Delta T^{300}$.2xV3^{m}.T (**Figure 33**) and pRAd-ORF6/G-PI (**Figure 36**) were linearized using appropriate restriction enzymes and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector Ad-$E^{m}\Delta C\Delta T^{300}$.2xV3^{m}.T/G-PI.

21) pRAd-ORF6-Gag/PI-RT

DNA sequence encoding the protease (PI) and reverse transcriptase (RT) from the *pol* region of HIV strain BH10 was inserted into a region downstream from the sequence encoding Gag in a shuttle vector pRAd-ORF6-Gag/PI-RT (**Figure 58**). As illustrated in **Figure 58**, Gag and PI-RT are expressed separately from a CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at two splicing acceptor sites, SA_1 and SA_2/SA_3.

The right shuttle vector pRAd-ORF6-Gag/PI-RT can be combined with any of the left shuttle vector (pLAd) described above to generate a recombinant adenoviral vector.

22) pRAd-ORF6-Gag-PI-RT

Alternatively, PI-RT was expressed as a fusion protein with Gag by inserting a C residue at position nt1410 to allow *pol* to be read within the same reading frame of *gag*. As illustrated in **Figure 59**, Gag and PI-RT are expressed from the same CMV promoter within the same reading frame. The resulting shuttle vector is designated as pRAd-ORF6-Gag-PI-RT.

The right shuttle vector pRAd-ORF6-Gag-PI-RT can be combined with any of the left shuttle vector (pLAd) described above to generate a recombinant adenoviral vector.

23) pRAd-ORF6-Gag/Pol

DNA sequence encoding the HIV enzymes PI, RT and IN from the *pol* region of HIV strain BH10 was inserted into a region downstream from the

sequence encoding Gag in a shuttle vector pRAd-ORF6-Gag/Pol (**Figure 60**). As illustrated in **Figure 60**, Gag and Pol are expressed separately from a CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at two splicing acceptor sites, SA_1 and SA_2/ SA_3.

The right shuttle vector pRAd-ORF6-Gag/Pol can be combined with any of the left shuttle vector (pLAd) described above to generate a recombinant adenoviral vector.

24) pRAd-ORF6-Gag-Pol

Alternatively, Pol was expressed as a fusion protein with Gag by inserting a C residue at position nt1410 to allow *pol* to be read within the same reading frame of *gag*. As illustrated in **Figure 61**, Gag and Pol are expressed from the same CMV promoter within the same reading frame. The resulting shuttle vector is designated as pRAd-ORF6-Gag-Pol.

The right shuttle vector pRAd-ORF6-Gag-Pol can be combined with any of the left shuttle vector (pLAd) described above to generate a recombinant adenoviral vector.

B. Immune responses of animals to the adenoviral vaccine against HIV antigens

Experimental mice were inoculated with the adoviral vaccine constructed above, Ad.tat.env.IL2 (also designated as "Ad-E.T.R/IL2" as described above, section A, subsection 1)), to elicit immune response to the HIV antigens expressed by this vector. Immunogenicity of the adenoviral vector was determined by measuring titers of antibody against HIV tat and env.

Figures 6 and **7** show the immunogenicity of Ad.tat.env.IL2 against the HIV Env protein in two groups of mice, respectively. These groups of C57BL/6 mice (supplied by Charles River Laboratories. Wilmington, MA) were injected intramuscularly with 10^7 pfu Ad.tat.env.IL2 on different dates as indicated in the figures. Blood (about 150-500 μl for each animal) was collected from four animals every two weeks following inoculation and serum was prepared. At 77 days post-inoculation, these mice were re-challenged with an additional 10^7 pfu of Ad.tat.env.IL2. Blood was collected from three animals every day following secondary challenge. Titers of antibody elicited

against HIV tat and env were determined by ELISA against Ad.tat.env.IL2-infected HeLa cell lysates.

Briefly, lysates of the HeLa cells infected with Ad.tat.env.IL2 were prepared as follows. HeLa cells were infected with Ad.tat.env.IL2 at a multiplicity of infection (MOI) of 20. Fourty-eight hours post infection, HeLa cells were harvested and resuspended in a buffer that contained 1% TritonX-100. A post-nuclear supernatant was obtained by centrifuging the lysates at 15,000 x g for 5 min. The lysates were diluted to 10 µg/ml for coating wells of ELISA plates. Standard ELISA assays were performed to measure OD450 of the sera and relative titers of antibody against HIV tat and env proteins were calculated by normalizing against the mean of the CD450 of mouse pre-immunization sera.

As shown in **Figure 6**, the three mice in this group had strong immune responses to the HIV antigens expressed by the adenoviral vector Ad.tat.env.IL2, with the highest titer of antibody against HIV antigens reached in about 42 days post inoculation. The second inoculation with Ad.tat.env.IL2 boosted the immune reponse again and very high titers were achieved within about 5 days of the second inoculation.

As shown in **Figure 7**, the three mice in this group also had strong immune responses to the HIV antigens expressed by the adenoviral vector Ad.tat.env.IL2, with the highest titer of antibody against HIV antigens reached in about 70 days post inoculation. The second inoculation with Ad.tat.env.IL2 boosted the immune reponse again and very high titers were achieved within about 5 days of the second inoculation.

Figures 12 A-B show the antibody production elicited by the recombinant adenoviral vectors Ad.3C.env.gag (also designated as "Ad-3C/$E^{m}\Delta C\Delta T^{300}$-G" as described above, section A, subsection 2)) in mice. C57BL/6 mice were injected intramuscularly with 10^{7} pfu Ad.3C.env.gag. At 77 days post-inoculation, these mice were re-challenged with an additional 10^{7} pfu Ad.3C.env.gag. Relative antibody titers of these mice were determined by ELISA against purified recombinant Gag (obtained from the NIH AIDS Research and Reference Reagent Program, Bethesda, MD) at week 10 post-immunization (or prime) (**Figure 12A**) and week 14 post-prime/week 3 post-boost (**Figure 12B**). As shown in **Figures 12A** and **12B**, the mice inoculated with Ad.3C.env.gag had strong immune responses to the HIV antigen Gag.

Figures 13 A-B show the antibody production elicited by the recombinant adenoviral vectors Ad.3C.env.rev.gag (also designated as "Ad-3C/E$^{m}\Delta C\Delta T^{99}$.T.R-G" as described above in section A, subsection 3)) in mice. C57BL/6 mice were injected intramuscularly with 10^7 pfu Ad.3C.env.rev.gag. At 77 days post-inoculation, these mice were re-challenged with an additional 10^7 pfu Ad.3C.env.rev.gag. Relative antibody titers of these mice were determined by ELISA against recombinant purified Gag at week 10 post-immunization (or prime) **(Figure 13A)** and week 14 post-prime/week 3 post-boost (**Figure 13B**). As shown in **Figures 13A** and **13B**, the mice inoculated with Ad.3C.env.rev.gag had strong immune responses to the HIV antigen Gag.

C. Activation of cytotoxic T lymphocytes (CTL) by immunization with the adenoviral vaccines against HIV antigens

Activation of cytotoxic T lymphocytes (CTL) by immunization with the adenoviral vaccine against HIV antigens was measured by using two independent assays: an IFNγ assay and a granzyme A assay. The IFNγ and granzyme assays were designed to detect antigen-specific activation of T-cells. IFNγ is secreted by activated CTL and T_H1 helper T cells which function specifically in the cellular immune pathway. Granzyme A is also secreted by activated CTL. The basic approach is to incubate splenocytes with target cells that express antigens of interest and look for secretion of IFNγ or granzyme A into the medium.

1) IFNγ assay

This assay is a modification of the standard ^{51}Cr-release lytic assay (Current Protocols in Immunology, Coligan et al., eds.) except that the target cells are not radiolabeled prior to incubation with the splenocytes. Detailed procedures for this assay are described in Di Fabio et al. (1994) "Quantitation of human influenza virus-specific cytotoxic T lymphocytes: correlation of cytotoxicity and increased numbers of IFN-gamma-(or IFNγ–) producing CD8+ T cells" Int. Immunol. 6:11-9. Briefly, about $1x10^6$ splenocytes were incubated with 10^5 target cells (e.g., infected with appropriate viruses carrying the target

antigens) in a total volume of 100 µl. Cells were incubated for 4h at 37°C. IFNγ was measured by ELISA from 25 µl medium.

Activation of CTL in mice inoculated with the adenoviral vaccine against HIV antigens was determined by using the IFNγ assay described above. Briefly, twelve C57BL/6 mice were injected intramuscularly with 10^7 pfu Ad.tat.env.IL2. Spleens were harvested from 4 inoculated mice at the time points indicated in **Figures 8A-C**. Splenocytes were activated by incubation with B16-F1 cells (a melanoma cell line from C57BL/6, ATCC No: CRL-6323) that had been infected with Ad.tat.env.IL2. At day seven after stimulation, activated splenocytes were mixed with B16-F1 cells infected with the indicated viruses. IFNγ secretion into the medium was determined by ELISA (R&D Systems, Minneapolis, MN).

Figures 8A-C show percent increases in the amount of IFNγ secreted into the medium over the period of time ranging from 4-8 weeks post inoculation. As shown in **Figure 8A**, secretion of IFNγ increased significantly in splenocytes of the four mice harvested 4 weeks post inoculation with Ad.tat.env.IL2. In contrast, little increase in IFNγ secretion occurred when the splenocytes were incubated with B16-F1 cells infected with an adenoviral vector expressing non-specifc protein β-Gal (Ad.lacZ) or uninfected B16-F1 cells.

Secrection of IFNγ increased more in the splenocytes of mice harvested 6 weeks post inoculation as shown in **Figure 8B**. Noticeably, there was near 100% increase in secrection of IFNγ in splenocytes of mouse 5 (**Figure 8B**).

Secrection of IFNγ increased more dramatically in the splenocytes of mice harvested 8 weeks post inoculation as shown in **Figure 8C**. There was more than 300% increase in secrection of IFNγ in splenocytes of mouse 11 (**Figure 8C**).

These results demonstrate that strong humoral immune responses against HIV, such as induction of high titer antibody and activation of CTL specifically targeting HIV antigens, have been achieved by inoculating animals with the adenoviral vaccine expressing both HIV viral antigens and an immuno-stimulator such as IL-2. The immune responses resemble those during a recovering of viral infection diseases. These results tend to show

that the genetic vaccines of the present invention that mimics natural viral infection hold great promises as efficacious vaccines for humans against HIV.

2) Granzyme A assay

Granzyme A assay was performed using a protocol modified from the one described in Deitz et al. (2000) "MHC I-dependent antigen presentation is inhibited by poliovirus protein 3A" Proc. Natl. Acad. Sci. 97:13790–13795. The granzyme A assay described in Deitz et al. was a modification of a protocol described in: Kane et al. (1989) "Cytolytic T-lymphocyte response to isolated class I H-2 proteins and influenza peptides" Nature (London) 340:157–159.

Granzyme A Assays were performed following similar procedures as for IFNγ assays with the following exceptions. Granzyme A secretion into the medium was determined by an enzymatic assay. Units of granzyme A were determined by calculating the slope of activity during the linear phase of the reaction. One unit of granzyme A was defined as the amount of enzyme required to convert the substrate to 1 OD_{405} in one hour.

Briefly, about $1x10^5$ activated splenocytes and about $1x10^5$ target cells were incubated together as for the IFNγ assays. Granzyme A activity was determined by combining 20 µl medium with 180 µl reaction mixture (0.2 mM BLT (N-α–benzyloxycarbonyl-L-lysinethiobenzyl ester, Sigma, St. Louis, MO), 0.22 mM DTNB (5,5'-dithio-bis(2-nitrobenzoicacid, Sigma, St. Louis, MO)) in 96-well plates and incubating at room temperature. Absorbance at 405 nm was monitored over a period of several hours. Slopes of enzyme activity were determined for the linear phase of the reaction and converted to units of enzyme.

Figure 9 shows increases in the amount of granzyme A secreted into the medium for splenocytes of mice harvested 8 weeks post inoculation. As shown in **Figure 9**, secretion of granzyme A increased significantly in splenocytes of the four mice harvested 8 weeks post inoculation with Ad.tat.env.IL2. In contrast, much less granzyme A secretion occurred when the splenocytes were incubated with B16-F1 cells infected with an adenoviral vector expressing non-specifc protein β-Gal (Ad.lacZ), an adenoviral vector expressing both hepatitis B surface antigen and IL-2 (Ad.HBsAg/IL2) or

uninfected B16-F1 cells. Similarly, there is little spontaneous granzyme A secretion in these splenocytes not incubated with the target cells.

Figure 14A shows the results of the granzyme A assays for series 1 mice at various time points indicated, including week 4, 6, 8 post-immunization and week 12/1, 13/2, 14/3 (prime/boost) post-secondary inoculation with Ad.3C.env.gag.

Figure 14B shows the results of the granzyme A assays for series 2 mice at various time points indicated, including week 2, 4, 6, 8 post-immunization with Ad.3C.env.gag.

These results, obtained by using the granzyme A assay independent from the IFNγ assay, again demonstrate that strong activation of CTL specifically targeting HIV antigens was induced by inoculating mice with the adenoviral vaccine expressing both HIV viral antigens and an immuno-stimulator such as IL-2. These results also support the belief that the genetic vaccines provided by the present invention hold great promises as efficacious vaccines for humans against HIV.

3) ELISPOT Assay

ELISPOT assays were performed to determine CTL activation in mice inoculated with the recombinant adenoviral vectors, Ad.3C.env.gag and Ad.3C.env.gag.rev. C57BL/6 mice were inoculated with 10^7 pfu Ad.3C.env.gag or Ad.3C.env.gag.rev. Mice were sacrificed at two-week intervals and splenocytes were prepared (see Current Protocols in Immunology, Coligan et al. eds.). At week 11, mice were inoculated with a second dose of 10^7 pfu of Ad.3C.env.gag or Ad.3C.env.gag.rev. 2×10^5 splenocytes were incubated with 4×10^4 MC57G cells (ATCC #CRL-2295) that had been infected with vaccinia viruses expressing either Env, Gag, or Rev, in 96-well, mouse IFNγ, ELISPOT plates (R&D Systems, Minneapolis, MN) for 30h. Non-specific activation was monitored following the addition of 4 μg/ml PHA (Sigma, St. Louis, MO) instead of antigen-expressing cells. IFNγ spots were visualized as per the kit instructions and counted. Wild type and recombinant vaccinia viruses were obtained from the NIH AIDS Research and Reference Reagent Program, Bethesda, MD.

Figures 15A shows the ELISPOT results for the four mice in serie1 at week 13/2 post-prime/boost with Ad.3C.env.gag. **Figures 15B** shows the

ELISPOT results for the four mice in serie1 at week 13/2 post-prime/boost with Ad.3C.env.rev.gag. These results indicate that immunization of mice with the genetic vaccines of the present invention induced strong activation of CTL against HIV Gag.

3. Genetic Vaccine Against Hepatitis B Virus

Embodiments of the genetic vaccine against hepatitis B virus and methods of their construction are described in detail as follows.

1) Construction of replication-defective adenoviral vaccines against hepatitis B virus

Two adenoviral vectors, Ad.HBsAg.IL2 and Ad.HBcAg.IL2, were constructed to carry the coding sequences for a hepatitis B surface antigen (HBsAg) and a HBV core antigen (HBcAg), respectively. In the same vector, DNA sequence encoding interleukin-2 (IL-2) was also included and expressed by a promoter different from that for expressing the viral antigen. This design is believed to be able to ensure high level expression of both the viral antigens and the immuno-stimulator IL-2 and to enhance immunogenicity of the adenoviral vaccine. As shown by experimental data presented in the next section, both of these two adenoviral vectors are capable of eliciting strong and long-lasting immune responses in animals against hepatitis B antigens.

These two adenoviral vectors, Ad.HBsAg.IL2 and Ad.HBcAg.IL2, were constructed using strategies similar to those for constructing the adenoviral vaccines against Ebola virus as described in detail above.

a) Ad.HBsAg.IL2

Briefly, full length HBsAg (with a silent mutation caused by deletion of Xba I site) was inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector pLAd (**Figure 4A**, left side), resulting in a shuttle vector pLAd-CMV-HBsAg.

The sequence encoding IL-2 (with a silent mutation caused by deletion of Xba I site) was inserted into E4 region of the adenoviral genome using the shuttle vector pRAd (**Figure 4A**, right side), resulting in a shuttle vector pRAd-CMV-IL2.

Both pLAd-CMV-HBsAg and pRAd-CMV-IL2 were linearized using appropriate restriction enzymes such as Xba I and EcoRI and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector designated Ad.HBsAg.IL2.

a) *Ad.HBcAg.IL2*

Briefly, sequences encoding full length HBsAg (with a silent mutation caused by deletion of Xba I site) and full length HBcAg were inserted into the left end (E1 region) of the adenoviral genome using a shuttle vector pLAd (**Figure 4A**, left side). HBsAg and HBcAg are expressed separately from another CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at two splicing acceptor sites, SA_1 and SA_2. The shuttle vector produced is designated pLAd-CMV-SD/SA_1-HBsAg-SA_2-HbcAg.

Sequences encoding multiple immuno-stimulators, including IL-2 (with a silent mutation caused by deletion of Xba I site), INF-γ, and GMCSF, were inserted into E4 region of the adenoviral genome using the shuttle vector pRAd (**Figure 4A**, right side). These three immuno-stimulators are expressed separately from another CMV promoter via a retroviral splicing donor (SD) and acceptor (SA) mechanism at three splicing acceptor sites, SA_1, SA_2, and SA_3. The shuttle vector produced is designated pRAd-CMV-SD/SA_1-IL2-SA_2- INFγ-SA_3-GMCSF.

Both pLAd-CMV-SD/SA_1-HBsAg-SA_2-HbcAg and pRAd-CMV-SD/SA_1-IL2-SA_2- INFγ-SA_3-GMCSF were linearized using appropriate restriction enzymes such as Xba I and EcoRI and ligated to the backbone of the adenovirus (**Figure 4B**), resulting in the recombinant adenoviral vector designated Ad.HBcAg.IL2.

2) Immune responses of animals to the adenoviral vaccines against HBV antigens

Experimental mice were inoculated with the adoviral vaccine constructed above, Ad.HBsAg.IL2 and Ad.HBcAg.IL2, to elicit immune response to the hepatitis B surface antigen and core antigen expressed by these two vectors, respectively. Immunogenicity of these adenoviral vectors

was determined by measuring titers of antibodies against HBsAg and HbcAg, respectively.

a) HBV surface antigen (HBsAg) antibody titers

CD-1 mice (Charles River Laboratories, Wilmington, MA) were injected intramuscularly with several different concentrations of Ad.HBsAg.IL2: 10^5, $1x10^6$, $1x10^7$, $1x10^8$, 5×10^5, 5×10^6, and 5×10^7 pfu virus. **Figure 10A** shows the relative Anti-HBsAg antibody titers measured for sera harvested from mice inoculated with 1×10^5 and 5×10^5 pfu. Serum in each measurement was diluted 1:500. **Figure 10B** shows the relative Anti-HbsAg antibody titers measured for sera harvested from mice inoculated with $1x10^7$ and $1x10^8$ pfu. Serum in each measurement was diluted 1:1500.

To measure the relative titers of the Anti-HbsAg antibody elicited by Ad.HBsAg.IL2, blood (about 150-500 µl) from each animal was collected from immunized mice every two weeks and serum was prepared. Blood was incubated at room temperature for 2-3 h to allow for clotting. The blood was then chilled overnight at 4°C to shrink the clot. Unclotted liquid was transferred to a clean tube and centrifuged at 2000 x g for 5 min. The supernatant was transferred to another clean tube. Sodium azide (NaN_3) was added to 0.05% as a preservative. Small aliquots were kept at 4°C for short-term storage. Long-term storage was at -80°C.

Relative anti-HBsAg titers were determined by ELISA against recombinant HBsAg purified from yeast (from Aldevron, LLC, Fargo, ND). As shown in **Figure 10A**, the mice in group 1 had increasingly strong immune responses to HBsAg expressed by the adenoviral vector, Ad.HBsAg.IL2, within 8 weeks post inoculation. This vector with a titer as low as 5×10^6 pfu was sufficient to elicit high levels of antibody specifically against HBsAg.

Figure 10B shows the immunogenicity of Ad.HBsAg.IL2 with higher titers. As shown in **Figure 10B**, immunogenicity of Ad.HBsAg.IL2 increased dramatically as the titer of the adenoviral vector was increased from 1×10^7 pfu to $1x\ 10^8$ pfu.

These results demonstrate that the adenoviral vector expressing both hepatitis B surface antigen and IL-2 can induce strong immune response specifically targeting the viral antigen in mice inoculated with this vector. These results also support the belief that the genetic vaccines provided by the

present invention hold great promises as efficacious vaccines for humans against hepatitis B virus.

b) HBV core antigen (HBcAg) antibody titers

Groups of C57BL/6 mice (Charles River Laboratories, Wilmington, MA) were injected intramuscularly with $1x10^7$ pfu Ad.HBcAg.IL2 on different dates. Blood was collected from four animals every two weeks following inoculation and serum was prepared. At 91 days (Group 3, **Figure 11A**) or 84 days (Group 4, **Figure 11B**) post-inoculation, mice were re-challenged with an additional $1x10^7$ pfu virus. Blood was collected from three animals every day following secondary challenge. Antibody titer was determined by ELISA against recombinant HBcAg purified from E. coli (from Chemicon International, Inc., Temecula, CA).

As shown in **Figure 11A**, mice in group 3 had strong immune response to the hepatitis core antigen HBcAg expressed by the adenoviral vector Ad.HBcAg.IL2, with the highest titer of antibody against HBcAg reached in about 28 days post inoculation. The second inoculation with Ad.HBcAg.IL2 boosted the immune reponse again and very high titers were achieved within about 3 days of the second inoculation.

As shown in **Figure 11B**, mice in group 4 also had strong immune response to the hepatitis core antigen HBcAg expressed by the adenoviral vector Ad.HBcAg.IL2, with the high titer of antibody against HBcAg reached in about 34 days post inoculation. The second inoculation with Ad.HBcAg.IL2 boosted the immune reponse again and very high titers were achieved within about 3 days of the second inoculation.

These results demonstrate that the adenoviral vector expressing both hepatitis B core antigen and IL-2 can also induce strong immune response specifically targeting the viral antigen in mice inoculated with this vector. These results once again support the belief that the genetic vaccines provided by the present invention hold great promises as efficacious vaccines for humans against hepatitis B virus.

CLAIMS

What is claimed is:

1. A recombinant adenovirus comprising:

an HIV sequence encoding an HIV antigen, expression of the HIV antigen by the recombinant adenovirus eliciting an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus.

2. The recombinant adenovirus of claim 1, wherein the recombinant adenovirus is replication-incompetent.

3. The recombinant adenovirus of claim 1, wherein the HIV antigen is an antigen of HIV-1 or HIV-2.

4. The recombinant adenovirus of claim 1, wherein the HIV antigen is an antigen of HIV strain BH10 or pNL4-3.

5. The recombinant adenovirus of claim 1, wherein the HIV antigen is an antigen of HIV clade A, B, C, D, E, F, or G.

6. The recombinant adenovirus of claim 1, wherein the HIV antigen is an HIV glycoprotein or surface antigen.

7. The recombinant adenovirus of claim 6, wherein the HIV glycoprotein is an HIV envelope protein.

8. The recombinant adenovirus of claim 7, wherein the HIV envelope protein is a wild type or mutant gp160, gp120, or gp41.

9. The recombinant adenovirus of claim 7, wherein the cleavage site of the HIV envelope protein is inactivated by mutation.

10. The recombinant adenovirus of claim 7, wherein the C-terminal cytosolic domain of the HIV envelope protein is deleted.

11. The recombinant adenovirus of claim 7, wherein both the cleavage site and the C-terminal cytosolic domain of the HIV envelope protein are deleted.

12. The recombinant adenovirus of claim 7, wherein the HIV envelop protein is encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 14, 16, 20, 21, 22, 23, and 24.

13. The recombinant adenovirus of claim 7, wherein the HIV sequence further encodes an HIV protein selected from the group consisting of RT, PR, Tat, Vif, Nef, and Rev.

14. The recombinant adenovirus of claim 7, wherein the HIV antigen is a modified HIV envelope protein that includes multiclade variable loops.

15. The recombinant adenovirus of claim 14, wherein the multiclade variable loops are V3 loops from at least two HIV clades.

16. The recombinant adenovirus of claim 15, wherein the at least two HIV clades are selected from the group consisting of clade A, B, C, D, E, F, and G of group M of HIV-1 isolates.

17. The recombinant adenovirus of claim 15, wherein the V3 loops are encoded by polynucleotides selected from the group consisting of SEQ ID NOs: 25, 26, 27, 28, 29, 30, and 31.

18. The recombinant adenovirus of claim 14, wherein the modified HIV envelope protein that includes multiclade variable loops is encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 32, 52, and 54.

19. The recombinant adenovirus of claim 1, further comprising:

a polynucleotide encoding a signal peptide that facilitates the secretion of the HIV antigen by a cell infected by the recombinant adenoviruse.

20. The recombinant adenovirus of claim 19, wherein the signal peptide is an HIV gp120 signal peptide.

21. The recombinant adenovirus of claim 19, wherein the signal peptide is encoded by SEQ ID NO: 74.

22. The recombinant adenovirus of claim 1, further comprising:
a polynucleotide encoding an membrane-anchoring domain that renders the HIV antigen bound to the surface of a cell infected by the recombinant adenoviruse.

23. The recombinant adenovirus of claim 22, wherein the membrane-anchoring domain is an HIV gp41 transmembrane domain.

24. The recombinant adenovirus of claim 22, wherein the membrane-anchoring domain is encoded by SEQ ID NO: 75.

25. The recombinant adenovirus of claim 1, wherein the HIV antigen is an HIV structural protein.

26. The recombinant adenovirus of claim 25, wherein the HIV structural protein is a wild type HIV Gag.

27. The recombinant adenovirus of claim 25, wherein the HIV structural protein is a proteolytic fragment of HIV Gag.

28. The recombinant adenovirus of claim 27, wherein the proteolytic fragment of HIV Gag is selected from the group consisting of p17/24, p17 and p24.

29. The recombinant adenovirus of claim 27, wherein the proteolytic fragment of HIV Gag is in a natural, secreted or membrane bound form.

30. The recombinant adenovirus of claim 27, wherein the proteolytic fragment of Gag is encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 34, 35, 36, 40, 41, 42, 46, 47, and 48.

31. The recombinant adenovirus of claim 1, further comprising:
a polynucleotide encoding an HIV protease or an HIV reverse transcriptase.

32. The recombinant adenovirus of claim 31, wherein the polynucleotide encoding an HIV protease is SEQ ID NO: 56.

33. The recombinant adenovirus of claim 31, wherein the HIV antigen is HIV Gag.

34. The recombinant adenovirus of claim 33, wherein the protease is expressed as a fusion protein with the HIV Gag.

35. The recombinant adenovirus of claim 33, wherein the protease is expressed separately from a promoter different from that for the HIV Gag.

36. The recombinant adenovirus of claim 33, wherein the protease is expressed as a separate protein from the same promoter for the HIV Gag via an IRES or splicing donor/acceptor mechanism.

37. The recombinant adenovirus of claim 1, further comprising:
a polynucleotide encoding a fusion protein of HIV protease and HIV reverse transcriptase.

38. The recombinant adenovirus of claim 37, wherein the HIV antigen is HIV Gag.

39. The recombinant adenovirus of claim 38, wherein the fusion protein of HIV protease and HIV reverse transcriptase is expressed as a fusion protein with the HIV Gag.

40. The recombinant adenovirus of claim 38, wherein the fusion protein of HIV protease and HIV reverse transcriptase is expressed separately from a promoter different from that for the HIV Gag.

41. The recombinant adenovirus of claim 38, wherein the fusion protein of HIV protease and HIV reverse transcriptase is expressed as a separate protein from the same promoter for the HIV Gag via an IRES or splicing donor/acceptor mechanism.

42. The recombinant adenovirus of claim 1, further comprising:
a polynucleotide encoding a fusion protein of HIV protease, HIV reverse transcriptase and HIV integrase.

43. The recombinant adenovirus of claim 42, wherein the HIV antigen is HIV Gag.

44. The recombinant adenovirus of claim 43, wherein the fusion protein of HIV protease, HIV reverse transcriptase and HIV integrase is expressed as a fusion protein with the HIV Gag.

45. The recombinant adenovirus of claim 43, wherein the fusion protein of HIV protease, HIV reverse transcriptase and HIV integrase is expressed separately from a promoter different from that for the HIV Gag.

46. The recombinant adenovirus of claim 43, wherein the fusion protein of HIV protease, HIV reverse transcriptase and HIV integrase is expressed as a separate protein from the same promoter for the HIV Gag via an IRES or splicing donor/acceptor mechanism.

47. The recombinant adenovirus of claim 1, further comprising:
an immuno-stimulator sequence heterologous to adenovirus and encoding an immuno-stimulator whose expression in the host enhances the immunogenicity of the HIV antigen.

48. The recombinant adenovirus of claim 47, wherein the HIV sequence is positioned in the E1 region of the adenovirus and the immuno-stimulator sequence is positioned in the E4 region of the adenovirus.

49. The recombinant adenovirus of claim 47, wherein both the HIV sequence and the immuno-stimulator sequence are positioned in the E1 or E4 region of the adenovirus, and are expressed from the same promoter bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

50. The recombinant adenovirus of claim 47, wherein the expression of the HIV antigen or the immuno-stimulator is controlled by an adenoviral promoter.

51. The recombinant adenovirus of claim 47, wherein the expression of the HIV antigen or the immuno-stimulator is controlled by a non-adenoviral promoter.

52. The recombinant adenovirus of claim 51, wherein the non-adenoviral promoter is selected from the group consisting of CMV promoter, SV40 promoter, retrovirus LTR promoter, and chicken cytoplasmic β-actin promoter.

53. The recombinant adenovirus of claim 47, wherein the immuno-stimulator is a cytokine.

54. The recombinant adenovirus of claim 53, wherein the cytokine is selected from the group consisting of interleukin-2, interleukin-4, interleukin-12, β- interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor, and granulocyte-macrophage colony stimulating factor.

55. The recombinant adenovirus of claim 47, wherein the immuno-stimulator is a combination of different cytokines.

56. The recombinant adenovirus of claim 55, wherein the combination of cytokines are expressed from the same promoter but as separate proteins via an IRES mechanism or a retroviral splicing donor/acceptor mechanism.

57. A recombinant adenovirus comprising:

a first HIV sequence encoding a first HIV antigen, expression of which is under the transcriptional control of a first promoter; and

a second HIV sequence encoding a second HIV antigen, expression of which is under the transcriptional control of a second promoter positioned in a different region than the first promoter,

expression of the first and second HIV sequences eliciting an immune response directed against the first and second HIV antigens upon infection of the host by the recombinant virus.

58. The recombinant adenovirus of claim 57, wherein the recombinant adenovirus is replication-incompetent.

59. The recombinant adenovirus of claim 57, wherein the first and second HIV antigens are the same.

60. The recombinant adenovirus of claim 57, wherein the first and second HIV antigens are different.

61. The recombinant adenovirus of claim 57, wherein the first or second HIV antigen is an HIV envelope protein.

62. The recombinant adenovirus of claim 61, wherein the HIV envelope protein is a wild type or mutant gp160, gp120, or gp41.

63. The recombinant adenovirus of claim 62, wherein the cleavage site of the HIV envelope protein is inactivated by mutation.

64. The recombinant adenovirus of claim 62, wherein the C-terminal cytosolic domain of the HIV envelope protein is deleted.

65. The recombinant adenovirus of claim 62, wherein both the cleavage site and the C-terminal cytosolic domain of the HIV envelope protein are deleted.

66. The recombinant adenovirus of claim 61, wherein the first or second HIV sequence further encodes an HIV protein selected from the group consisting of RT, PR, Tat, Vif, Nef, and Rev.

67. The recombinant adenovirus of claim 57, wherein the first or second HIV antigen is a modified HIV envelope protein that includes multiclade variable loops.

68. The recombinant adenovirus of claim 67, wherein the multiclade variable loops are V3 loops from at least two HIV clades.

69. The recombinant adenovirus of claim 68, wherein the at least two HIV clades are selected from the group consisting of clade A, B, C, D, E, F, and G of group M of HIV-1 isolates.

70. The recombinant adenovirus of claim 68, wherein the V3 loops are encoded by polynucleotides selected from the group consisting of SEQ ID NOs: 25, 26, 27, 28, 29, 30, and 31.

71. The recombinant adenovirus of claim 57, further comprising:
a polynucleotide encoding a signal peptide that facilitates the secretion of the first or second HIV antigen by a cell infected by the recombinant adenoviruse.

72. The recombinant adenovirus of claim 71, wherein the signal peptide is an HIV gp120 signal peptide.

73. The recombinant adenovirus of claim 71, wherein the signal peptide is encoded by SEQ ID NO: 74.

74. The recombinant adenovirus of claim 57, further comprising:
a polynucleotide encoding an membrane-anchoring domain that renders the first or second HIV antigen bound to the surface of a cell infected by the recombinant adenoviruse.

75. The recombinant adenovirus of claim 74, wherein the membrane-anchoring domain is an HIV gp41 transmembrane domain.

76. The recombinant adenovirus of claim 74, wherein the membrane-anchoring domain is encoded by SEQ ID NO: 75.

77. The recombinant adenovirus of claim 57, wherein the first and second HIV antigen is an HIV structural protein.

78. The recombinant adenovirus of claim 77, wherein the HIV structural protein is a wild type HIV Gag.

79. The recombinant adenovirus of claim 77, wherein the HIV structural protein is a proteolytic fragment of HIV Gag.

80. The recombinant adenovirus of claim 77, wherein the proteolytic fragment of HIV Gag is selected from the group consisting of p17/24, p17 and p24.

81. The recombinant adenovirus of claim 77, wherein the proteolytic fragment of HIV Gag is in a natural, secreted or membrane bound form.

82. The recombinant adenovirus of claim 77, wherein the proteolytic fragment of Gag is encoded by a polynucleotide selected from the group consisting of SEQ ID NOs: 34, 35, 36, 40, 41, 42, 46, 47, and 48.

83. The recombinant adenovirus of claim 77, further comprising:
a polynucleotide encoding an HIV protease.

84. The recombinant adenovirus of claim 83, wherein the polynucleotide encoding an HIV protease is SEQ ID NO: 56.

85. The recombinant adenovirus of claim 57, wherein the first HIV antigen is a wildtype or mutant HIV envelope protein, and the second HIV antigen is a wildtype or mutant HIV structural protein.

86. The recombinant adenovirus of claim 85, wherein wildtype or mutant HIV structural protein is wildtype Gag or a proteolytic fragment of Gag.

87. The recombinant adenovirus of claim 57, wherein both the first and second HIV antigen are a wildtype or mutant HIV envelope protein.

88. The recombinant adenovirus of claim 57, wherein both the first and second HIV antigen are a wildtype or mutant HIV structural protein.

89. The recombinant adenovirus of claim 57, further comprising:
an immuno-stimulator sequence heterologous to adenovirus and encoding an immuno-stimulator whose expression in the host enhances the immunogenicity of the first or second HIV antigen.

90. The recombinant adenovirus of claim 89, wherein the first or second HIV sequence and the immuno-stimulator sequence are expressed from the same promoter bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

91. The recombinant adenovirus of claim 89, wherein the immuno-stimulator is a cytokine.

92. The recombinant adenovirus of claim 91, wherein the cytokine is selected from the group consisting of interleukin-2, interleukin-4, interleukin-12, β- interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor, and granulocyte-macrophage colony stimulating factor.

93. The recombinant adenovirus of claim 57, wherein the first or second promoter is an adenoviral promoter.

94. The recombinant adenovirus of claim 57, wherein the first or second promoter is non-adenoviral promoter.

95. The recombinant adenovirus of claim 94, wherein the non-adenoviral promoter is selected from the group consisting of CMV promoter, SV40 promoter, retrovirus LTR promoter, and chicken cytoplasmic β-actin promoter.

96. The recombinant adenovirus of claim 57, wherein the first promoter is in the E1 region of the adenovirus and the second promoter is positioned in the E4 region of the adenovirus.

97. A method for enhancing the immunity of a host to HIV infection, comprising:

administering to the host a first recombinant adenovirus comprising a first HIV sequence encoding a first HIV antigen, expression of the first HIV antigen by the first recombinant adenovirus eliciting an immune response directed against the first HIV antigen in a host upon infection of the host by the recombinant adenovirus.

98. The method of claim 97, wherein administering to the host a recombinant adenovirus is performed intramuscularly, intratracheally, subcutaneously, intranasally, intradermally, rectally, orally or parentally.

99. The method of claim 97, wherein the recombinant adenovirus further comprises one or more immuno-stimulator sequences heterologous to adenovirus that encodes an immuno-stimulator whose expression in the host enhances the immunogenicity of the HIV antigen.

100. The method of claim 97, further comprising:

administering to the host an immuno-stimulator.

101. The method of claim 100, wherein the immuno-stimulator is a cytokine selected from the group consisting of interleukin-2, interleukin-4, interleukin-12, β- interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor, and granulocyte-macrophage colony stimulating factor.

102. The method of claim 97, further comprising:

administering to the host a second recombinant adenovirus of different serotype than that of the first recombinant adenovirus and comprising a second HIV sequence encoding a second HIV antigen, expression of the second HIV antigen by the second recombinant adenovirus eliciting an immune response directed against the second HIV antigen in a host upon infection of the host by the recombinant adenovirus.

103. The method of claim 102, wherein the serotype of the first recombinant adenovirus is adenovirus serotype 5, and the serotype of the second recombinant adenovirus is selected from the group consisting of adenovirus serotype 1-4 and 6-51.

104. The method of claim 102, wherein the first HIV antigen encoded by the first recombinant adenovirus is the same as the second HIV antigen encoded by the second recombinant adenovirus.

105. The method of claim 102, wherein the first HIV antigen encoded by the first recombinant adenovirus is different from the second HIV antigen encoded by the second recombinant adenovirus.

106. The method of claim 102, wherein the second recombinant adenovirus has the same adenoviral backbone as the first one except that the fiber region of the second recombinant adenovirus is of different serotype than that in the first recombinant adenovirus.

107. The method of claim 102, wherein the second recombinant adenovirus has the same adenoviral backbone as the first one except that the knob, shaft, or penton base domain of the fiber region of the second recombinant adenovirus is of different serotype than the corresponding one in the first recombinant adenovirus.

108. The method of claim 102, wherein the second recombinant adenovirus is administered to the host at least one week post the administration of the first recombinant adenovirus.

109. The method of claim 97, further comprising:
harvesting serum from the host after the administration of the first recombinant adenovirus.

110. The method of claim 109, wherein the host is a human or a non-human primate.

111. The method of claim 109, further comprising:
storing the serum for at least 12 hour; and
then administering the serum to the host or another host.

112. The method of claim 111, wherein the other host is a human or a non-human primate.

113. The method of claim 97, further comprising:
isolating antibody against the first HIV antigen from the host after the administration of the first recombinant adenovirus; and
then administering the antibody to host or another host.

114. A method of enhancing the immunity of a host to HIV infection, comprising:
administering to the host a recombinant adenovirus comprising
a first HIV sequence encoding a first HIV antigen, expression of which is under the transcriptional control of a first promoter; and
a second HIV sequence encoding a second HIV antigen, expression of which is under the transcriptional control of a second promoter positioned in a different region than the first promoter,
expression of the first and second HIV sequences eliciting an immune response directed against the first and second HIV antigens upon infection of the host by the recombinant virus.

115. The method of claim 114, further comprising:

administering to the host the recombinant adenovirus at least once again after the initial administration of the recombinant adenovirus.

116. A method for enhancing the immunity of a host to infection of a first and second pathogenic virus, comprising:

administering to the host a first recombinant adenovirus comprising a first antigen sequence heterologous to native adenovirus and encoding a first viral antigen from the first pathogenic virus, expression of the first viral antigen by the first recombinant adenovirus eliciting an immune response directed against the first viral antigen in a host upon infection of the host by the first recombinant adenovirus; and

administering to the host a second recombinant adenovirus comprising a second antigen sequence heterologous to native adenovirus and encoding a second viral antigen from the second pathogenic virus, expression of the second viral antigen by the second recombinant adenovirus eliciting an immune response directed against the second viral antigen in a host upon infection of the host by the first recombinant adenovirus.

117. The method of claim 116, wherein administering to the host the first or second recombinant adenovirus is performed intramuscularly, intratracheally, subcutaneously, intranasally, intradermally, rectally, orally or parentally.

118. The method of claim 116, wherein the serotype of the first recombinant adenovirus is adenovirus serotype 5, and the serotype of the second recombinant adenovirus is selected from the group consisting of adenovirus serotype 1-4 and 6-51.

119. The method of claim 116, wherein the first viral antigen encoded by the first recombinant adenovirus is the same as the second viral antigen encoded by the second recombinant adenovirus.

120. The method of claim 116, wherein the first viral antigen encoded by the first recombinant adenovirus is different from the second viral antigen encoded by the second recombinant adenovirus.

121. The method of claim 116, wherein the second recombinant adenovirus has the same adenoviral backbone as the first one except that the fiber region of the second recombinant adenovirus is of different serotype than that in the first recombinant adenovirus.

122. The method of claim 116, wherein the second recombinant adenovirus has the same adenoviral backbone as the first one except that the knob, shaft, or penton base domain of the fiber region of the second recombinant adenovirus is of different serotype than the corresponding one in the first recombinant adenovirus.

123. The method of claim 116, wherein the second recombinant adenovirus has the same adenoviral backbone as the first one except that the knob domain of the fiber region of the second recombinant adenovirus is of different serotype than the corresponding one in the first recombinant adenovirus.

124. The method of claim 116, wherein the second recombinant adenovirus is administered to the host at least one week post the administration of the first recombinant adenovirus.

125. The method of claim 116, wherein the first or second recombinant adenovirus is replication-incompetent.

126. The method of claim 116, wherein the first recombinant virus further comprises a third antigen sequence heterologous to native adenovirus and encoding a third viral antigen from the first or second pathogenic virus.

127. The method of claim 126, wherein the first and third antigen sequences are positioned in the E1 and E3 or E4 region of the native progenitor of the first recombinant adenovirus, respectively.

128. The method of claim 126, wherein the first and third antigen sequences are expressed bicistronically by the same promoter.

129. The method of claim 128, wherein the first and second antigen sequences are expressed bicistronically via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

130. The method of claim 116, wherein

the first recombinant virus further comprises a third antigen sequence heterologous to native adenovirus and encoding a third viral antigen from the first or second pathogenic virus, and

the second recombinant virus further comprises a fourth antigen sequence heterologous to native adenovirus and encoding a fourth viral antigen from the first or second pathogenic virus.

131. The method of claim 130, wherein the first and third antigen sequences are positioned in the E1 and E3 or E4 region of the native progenitor of the first recombinant adenovirus, respectively; and the second and fourth antigen sequence are positioned in the E1 and E3 or E4 region of the native progenitor of the second recombinant adenovirus, respectively.

132. The method of claim 131, wherein the first and third antigen sequences are expressed bicistronically by the same promoter, or the second and fourth antigen sequences are expressed bicistronically by the same promoter,

133. The method of claim 132, wherein the bicistronic expression is via an internal ribosomal entry site or via a splicing donor-acceptor mechanism.

134. The method of claim 116, wherein the first and the second pathogenic viruses are the same.

135. The method of claim 116, wherein the first and the second pathogenic viruses are of the same type but of different subtype or clade.

136. The method of claim 116, wherein the first and the second pathogenic viruses are different types of the same virus.

137. The method of claim 116, wherein the first and the second pathogenic viruses are different viruses.

138. The method of claim 116, wherein the first or second pathogenic virus is a human immunodeficiency virus.

139. The method of claim 138, wherein the first or second viral antigen is an HIV surface, core/capsid, regulatory, enzyme or accessory protein.

140. The method of claim 138, wherein the first or second viral antigen is selected from the group consisting of HIV gp120, gp41, Gag, p17, p24, p2, p7, p1, p6, Tat, Rev, PR, RT, IN, Vif, Vpr, Vpx, Vpu and Nef.

141. The method of claim 116, wherein the first or second pathogenic virus is influenza virus.

142. The method of claim 141, wherein the first or second viral antigen is a glycoprotein of the influenza virus.

143. The method of claim 142, wherein the first or second viral antigen is influenza glycoprotein HA1, HA2 or NA.

144. The method of claim 116, wherein the first or second pathogenic virus is Ebola virus.

145. The method of claim 144, wherein the first or second viral antigen is an Ebola glycoprotein.

146. The method of claim 145, wherein the first or second viral antigen is Ebola GP1 or GP2 protein.

147. The method of claim 146, wherein the first or second viral antigen is an Ebola nucleocapsid protein.

148. The method of claim 116, wherein the first or second pathogenic virus is Marburg virus.

149. The method of claim 148, wherein the first or second viral antigen is a Marburg glycoprotein.

150. The method of claim 148, wherein the first or second viral antigen is a Marburg nucleocapsid protein.

151. The method of claim 116, wherein the first or second pathogenic virus is Arbovirus.

152. The method of claim 151, wherein the first or second viral antigen is Arbovirus glycoprotein.

153. The method of claim 116, wherein the first or second pathogenic virus is hepatitis virus.

154. The method of claim 153, wherein the hepatitis virus is hepatitis A, B, C, D or E virus.

155. The method of claim 153, wherein the first or second viral antigen is surface antigen or core protein of hepatitis B virus.

156. The method of claim 155, wherein the first or second viral antigen is SHBsAg, MHBsAg, or LHBsAg of hepatitis B virus.

157. The method of claim 153, wherein the first or second viral antigen is a surface antigen or core protein of hepatitis C virus.

158. The method of claim 157, wherein the first or second viral antigen is NS3, NS4 or NS5 antigen of hepatitis C virus.

159. The method of claim 116, wherein the first or second pathogenic virus is respiratory syncytial virus.

160. The method of claim 159, wherein the first or second viral antigen is a glycoprotein or a fusion protein of respiratory syncytial virus

161. The method of claim 116, wherein the first or second pathogenic virus is herpes simplex virus.

162. The method of claim 161, wherein the first or second pathogenic virus is herpes simplex virus type-1 or type-2.

163. The method of claim 161, wherein the first or second viral antigen is glycoprotein D from herpes simplex virus type-2.

164. The method of claim 116, wherein the first or second pathogenic virus is human papilloma virus.

165. The method of claim 164, wherein the first or second viral antigen is E6 or E7 of human papilloma virus.

166. The method of claim 116, wherein the first or second viral antigen is a full-length antigenic viral protein or a portion of the antigenic viral protein that contains the predominant antigen, neutralizing antigen, or epitope of the first or second pathogenic virus.

167. The method of claim 116, wherein the first or second viral antigen is a modified antigen that is mutated from a glycoprotein of the first or second pathogenic virus such that the first or second viral antigen is rendered non-functional as a viral component but retains its antigenicity.

168. The method of claim 167, wherein the modification of first or second viral antigen includes deletions in the proteolytic cleavage site of the glycoprotein, and duplications and rearrangement of immunosuppressive peptide regions of the glycoprotein.

169. The method of claim 116, wherein the first or second recombinant adenovirus further comprises:

an immuno-stimulator sequence that is heterologous to native adenovirus and encodes an immuno-stimulator.

170. The method of claim 169, wherein the immuno-stimulator is a cytokine.

171. The method of claim 170, wherein the cytokine is selected from the group consisting of interleukin-2, interleukin-4, interleukin-12, β- interferon, λ-interferon, γ-interferon, granulocyte colony stimulating factor, and granulocyte-macrophage colony stimulating factor.

172. The method of claim 116, further comprising:
harvesting serum from the host after the administration of the first and second recombinant adenovirus.

173. The method of claim 172, wherein the host is a human or a non-human primate.

174. The method of claim 172, further comprising:
storing the serum for at least 12 hour; and
then administering the serum to the host or another host.

175. The method of claim 174, wherein the other host is a human or a non-human primate.

176. The method of claim 116, further comprising:
isolating antibody against the first or second viral antigen from the host after the administration of the first and second recombinant adenovirus; and
then administering the antibody to host or another host.

177. The method of claim 176, wherein the host or the other host is a human or a non-human primate.

FIGURE 1A

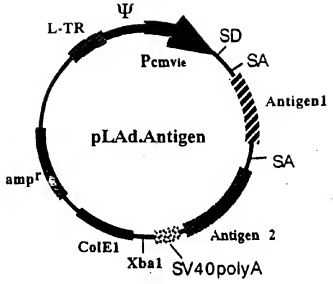


FIGURE 1B

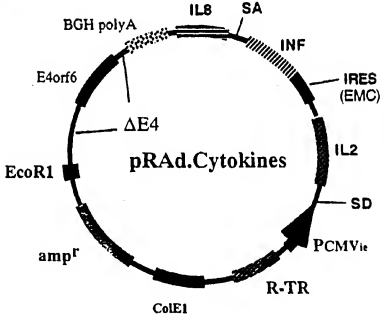


FIGURE 1C

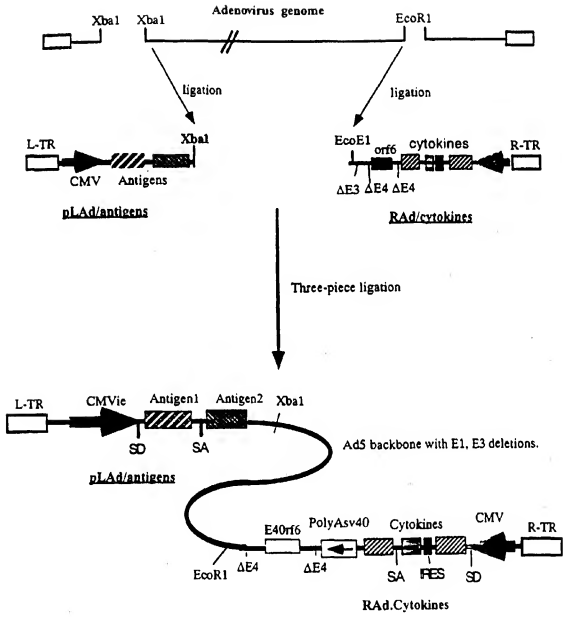
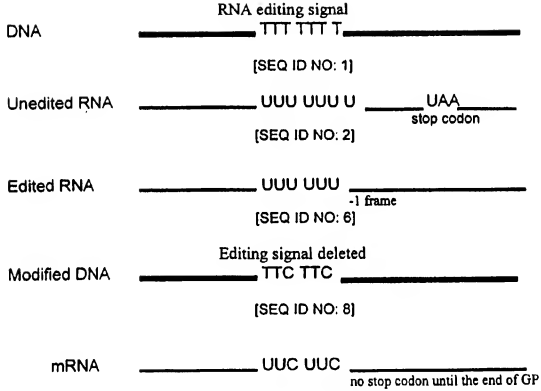

Adenovirus genome
Xba1
Xba1
EcoR1
ligation
ligation
L-TR
Xba1
CMV
Antigens
pLAd/antigens
EcoE1
orf6
cytokines
R-TR
ΔE3 ΔE4 ΔE4
RAd/cytokines
Three-piece ligation
L-TR
CMVie
Antigen1
Antigen2
Xba1
SD
SA
pLAd/antigens
Ad5 backbone with E1, E3 deletions.
E40rf6
PolyAsv40
Cytokines
CMV
R-TR
EcoR1
ΔE4
ΔE4
SA
IRES
SD
RAd.Cytokines

FIGURE 2


RNA editing signal
DNA
TTT TTT T
[SEQ ID NO: 1]
Unedited RNA
UUU UUU U
UAA
stop codon
[SEQ ID NO: 2]
Edited RNA
UUU UUU
-1 frame
[SEQ ID NO: 6]
Editing signal deleted
Modified DNA
TTC TTC
[SEQ ID NO: 8]
mRNA
UUC UUC
no stop codon until the end of GP
[SEQ ID NO: 7]

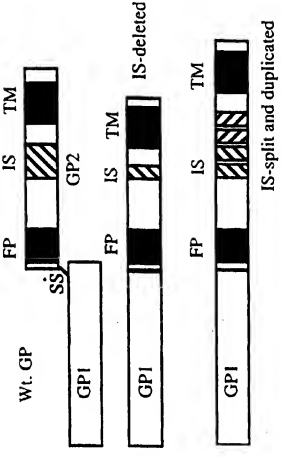


FIGURE 3A

FIGURE 3B

FIGURE 3C

FIGURE 4A

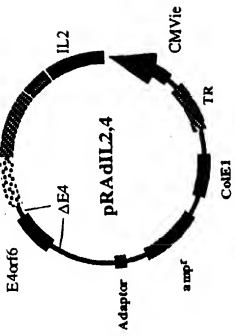

pRAdIL2,4
IL2
CMVie
TR
ColE1
amp^r
Adaptor
E4orf6
ΔE4
BGH polyA
IL4
pLAd/EBO-GP
Pcmvie
GP
Adaptor
ColE1
amp^r
TR

FIGURE 4B

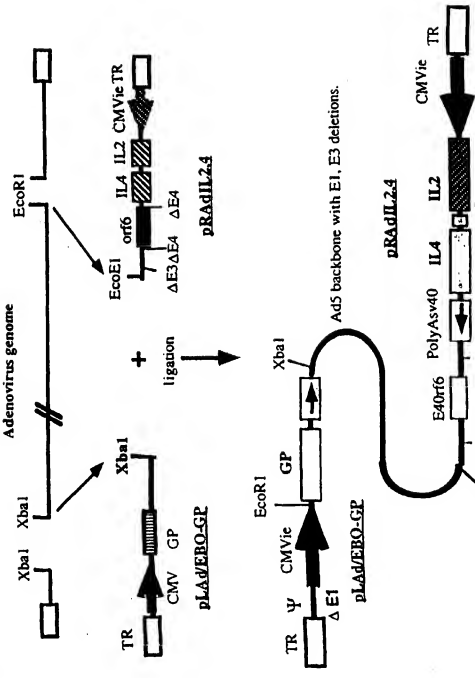
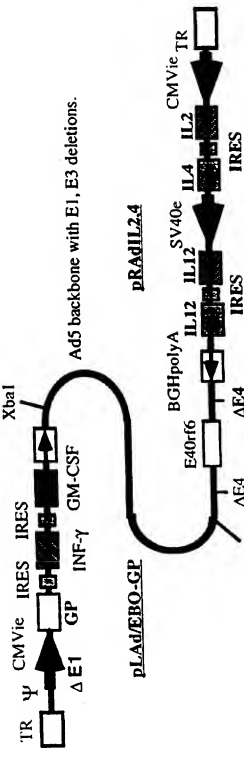

Adenovirus genome
EcoR1
Xba1
Xba1
TR
Ψ
Δ E1
CMVie
CMV
GP
pLAd/EBO-GP
EcoR1
Xba1
GP
+
ligation
EcoE1
orf6
IL4
IL2
CMVie TR
ΔE3ΔE4
ΔE4
pRAdIL2.4
Xba1
Ad5 backbone with E1, E3 deletions.
pLAd/EBO-GP
pRAdIL2.4
E40rf6
PolyAsv40
IL4
IL2
IRES
CMVie
TR
ΔE4
ΔE4
EcoR1

FIGURE 5


TR
Ψ
CMVie
ΔE1
GP
IRES
INF-γ
IRES
GM-CSF
Xba1
pLAdEBO-GP
Ad5 backbone with E1, E3 deletions.
pRAdIL2.4
E40rf6
BGHpolyA
ΔE4
ΔE4
EcoR1
IL12
IL12
IRES
SV40e
IL4
IL2
IRES
CMVie
TR

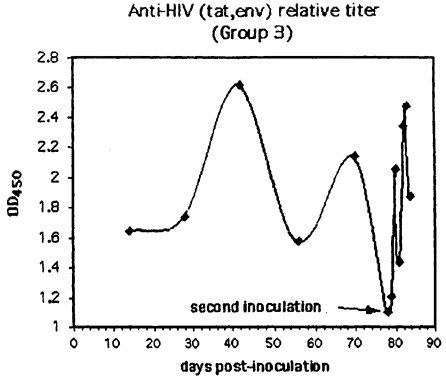

Anti-HIV (tat,env) relative titer
(Group 3)
OD450
2.8
2.6
2.4
2.2
2
1.8
1.6
1.4
1.2
1
second inoculation
0
10
20
30
40
50
60
70
80
90
days post-inoculation

FIGURE 6

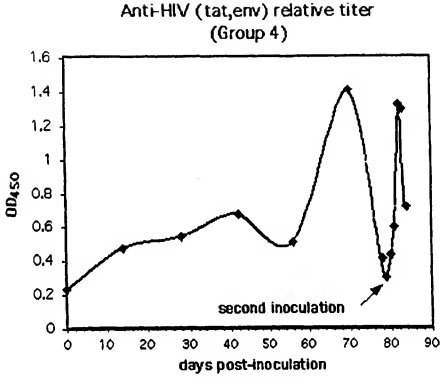

Anti-HIV (tat,env) relative titer
(Group 4)
OD450
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 10 20 30 40 50 60 70 80 90
days post-inoculation
second inoculation

FIGURE 7

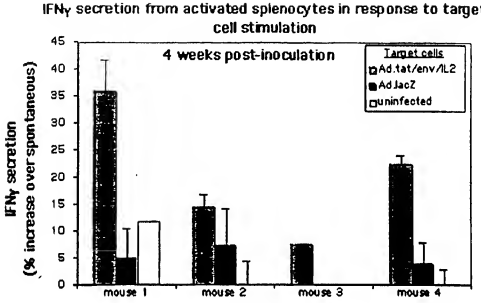

IFNγ secretion from activated splenocytes in response to target cell stimulation
4 weeks post-inoculation
Target cells
Ad.tat/env/IL2
AdJacZ
uninfected
IFNγ secretion (% increase over spontaneous)
45
40
35
30
25
20
15
10
5
0
mouse 1
mouse 2
mouse 3
mouse 4

FIGURE 8A

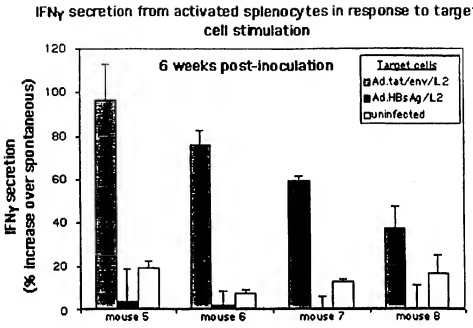

IFNγ secretion from activated splenocytes in response to target cell stimulation
6 weeks post-inoculation
Target cells
Ad.tat/env/L2
Ad.HBsAg/L2
uninfected
IFNγ secretion (% increase over spontaneous)
120
100
80
60
40
20
0
mouse 5
mouse 6
mouse 7
mouse 8

FIGURE 8B

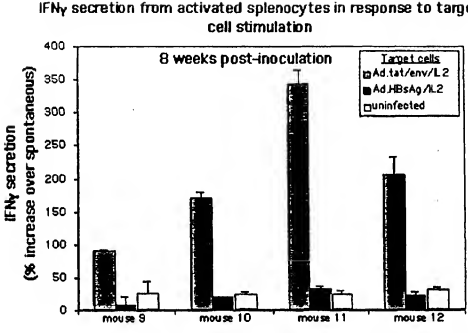

IFNγ secretion from activated splenocytes in response to target cell stimulation
8 weeks post-inoculation
Target cells
Ad.tat/env/IL2
Ad.HBsAg/IL2
uninfected
IFNγ secretion (% increase over spontaneous)
400
350
300
250
200
150
100
50
0
mouse 9
mouse 10
mouse 11
mouse 12

FIGURE 8C

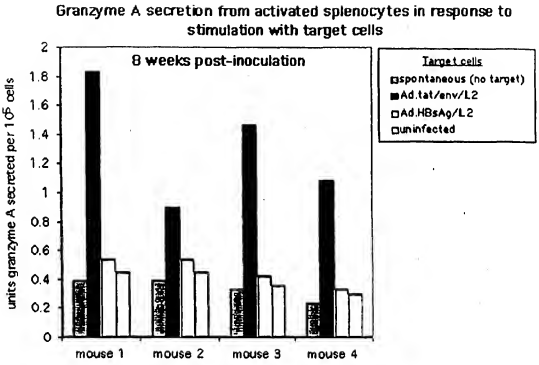

Granzyme A secretion from activated splenocytes in response to stimulation with target cells
8 weeks post-inoculation
units granzyme A secreted per 10^5 cells
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
mouse 1
mouse 2
mouse 3
mouse 4
Target cells
spontaneous (no target)
Ad.tat/env/L2
Ad.HBsAg/L2
uninfected

FIGURE 9

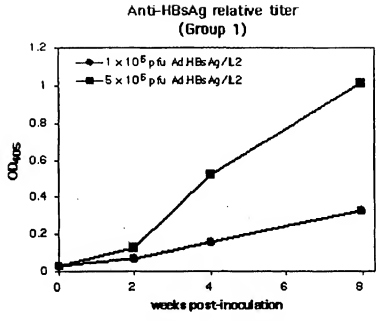


FIGURE 10A

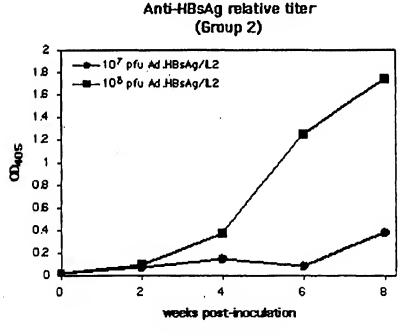


FIGURE 10B

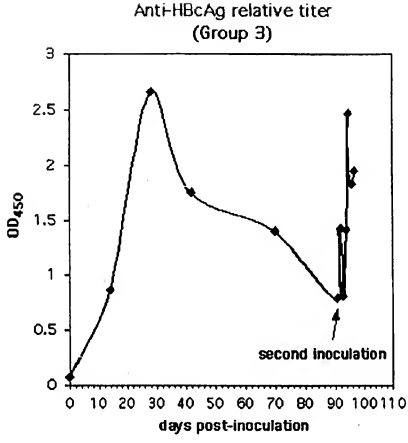

Anti-HBcAg relative titer
(Group 3)
OD450
3
2.5
2
1.5
1
0.5
0
0 10 20 30 40 50 60 70 80 90 100 110
days post-inoculation
second inoculation

FIGURE 11A

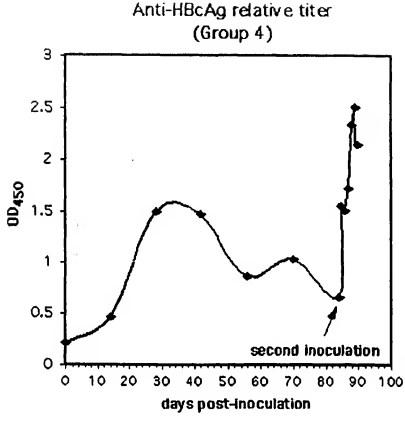
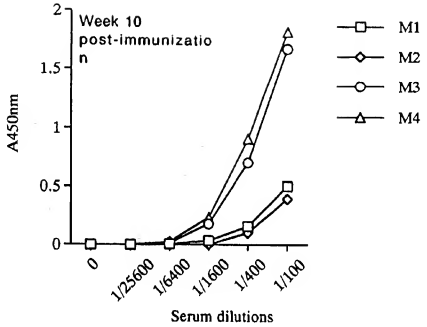

Anti-HBcAg relative titer
(Group 4)
OD450
3
2.5
2
1.5
1
0.5
0
second inoculation
0 10 20 30 40 50 60 70 80 90 100
days post-inoculation

FIGURE 11B

FIGURE 12

A.


Week 10
post-immunizatio
n
A450nm
2
1.5
1
0.5
0
0
1/25600
1/6400
1/1600
1/400
1/100
Serum dilutions
M1
M2
M3
M4

B.

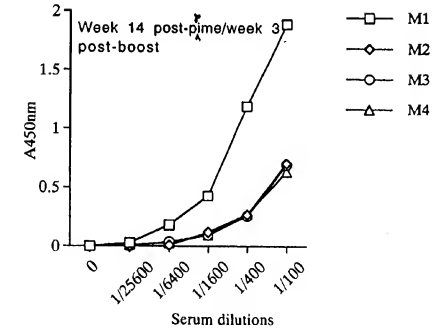
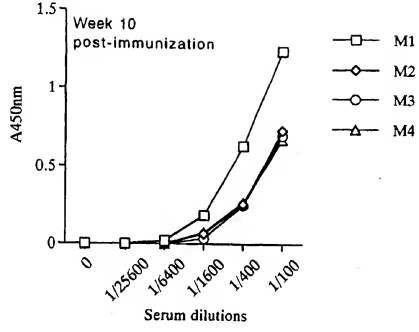

Week 14 post-prime/week 3
post-boost
A450nm
2
1.5
1
0.5
0
0
1/25600
1/6400
1/1600
1/400
1/100
Serum dilutions
M1
M2
M3
M4

FIGURE 13

A.


Week 10
post-immunization
A450nm
1.5
1
0.5
0
0
1/25600
1/6400
1/1600
1/400
1/100
Serum dilutions
M1
M2
M3
M4

B.

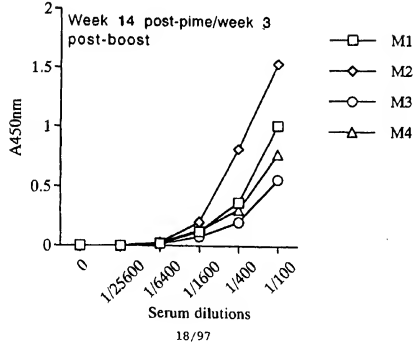

Week 14 post-pime/week 3
post-boost
A450nm
2
1.5
1
0.5
0
0
1/25600
1/6400
1/1600
1/400
1/100
Serum dilutions
M1
M2
M3
M4

FIGURE 14

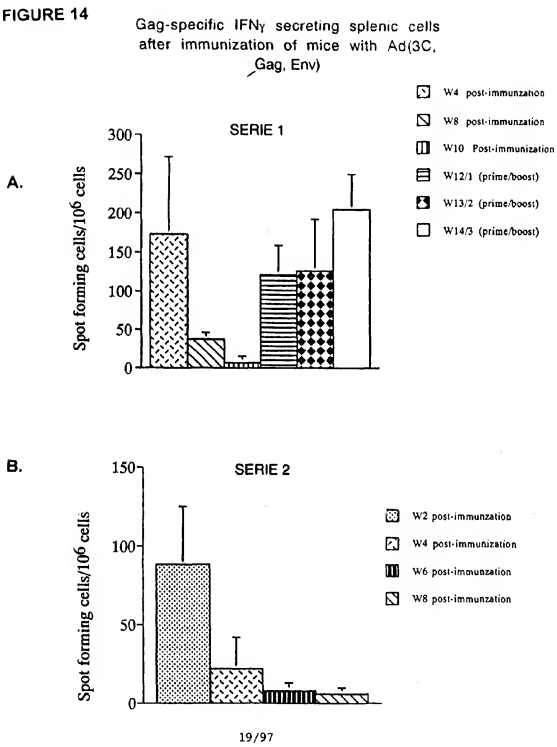
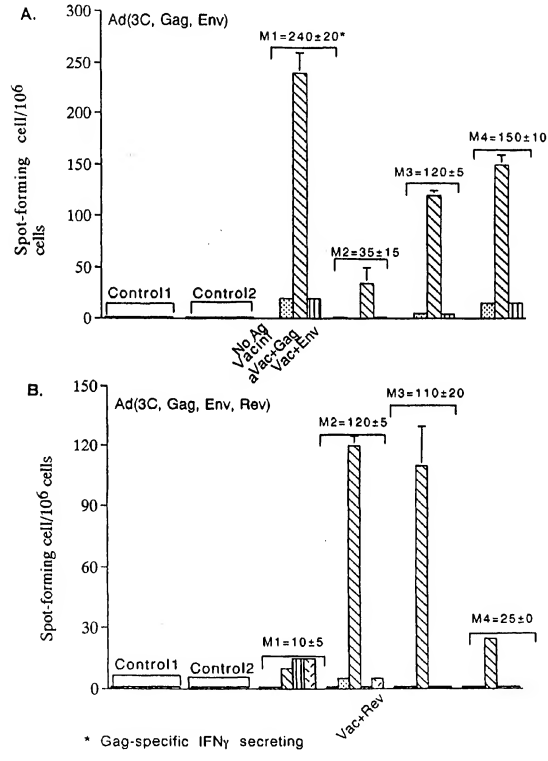

Gag-specific IFNγ secreting splenic cells after immunization of mice with Ad(3C, Gag, Env)
A.
SERIE 1
Spot forming cells/10^6 cells
300
250
200
150
100
50
0
W4 post-immunzation
W8 post-immunzation
W10 Post-immunization
W12/1 (prime/boost)
W13/2 (prime/boost)
W14/3 (prime/boost)
B.
SERIE 2
Spot forming cells/10^6 cells
150
100
50
0
W2 post-immunzation
W4 post-immunzation
W6 post-immunzation
W8 post-immunzation

FIGURE 15 L23: ELISPOT for IFNγ secretion: Serie1 spleen cells from mice at week W13/2 (post-prime/boost)



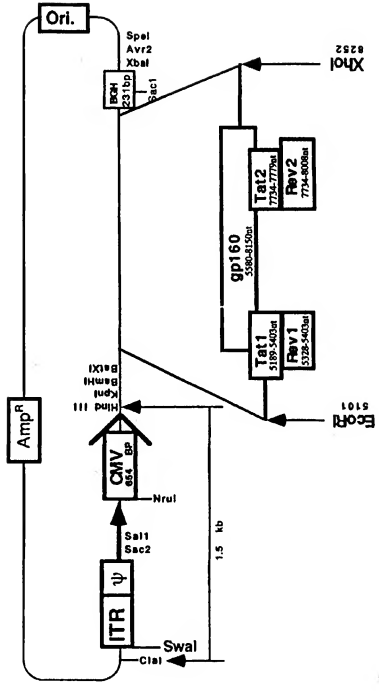


FIGURE 16A

pLAd-E.T.R

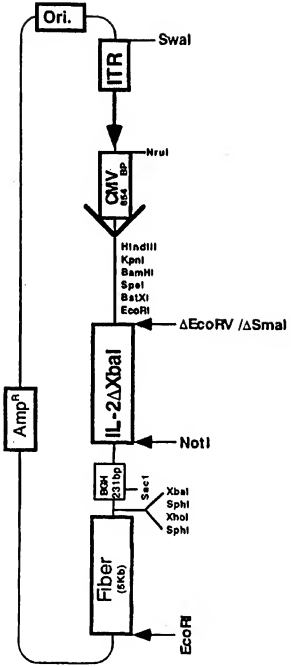


FIGURE 16B

pRAd.ORF6-IL2

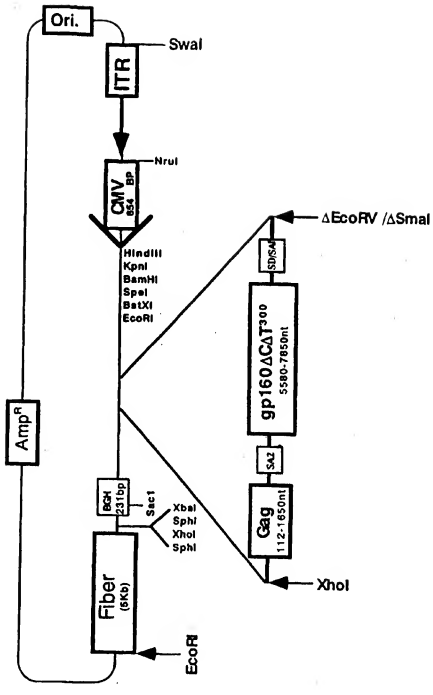


FIGURE 17A

pRAd.ORF6-E^{III}ΔCΔT^{300}-G

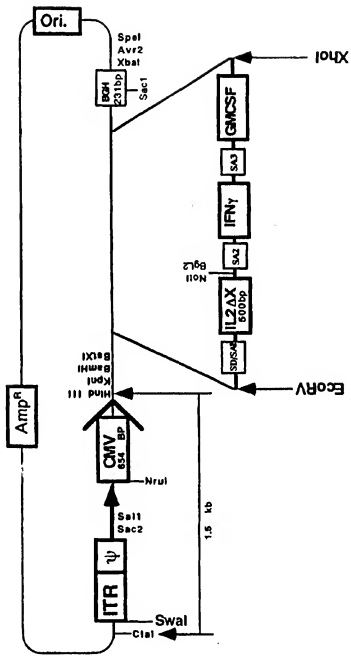
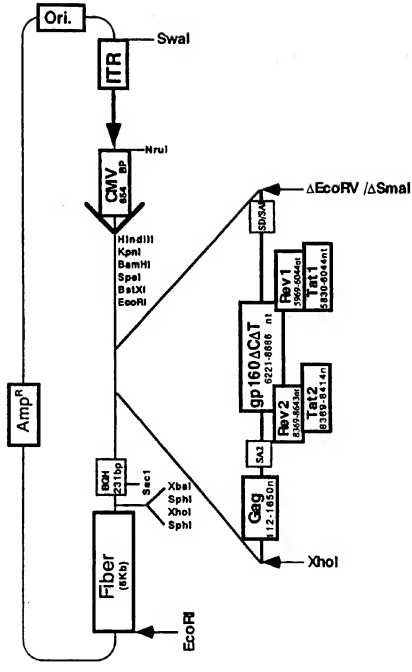


FIGURE 17B

pLAd-3C

FIGURE 18

pRAd.ORF6-E^{m}-ΔCΔT^{99}.T.R-G



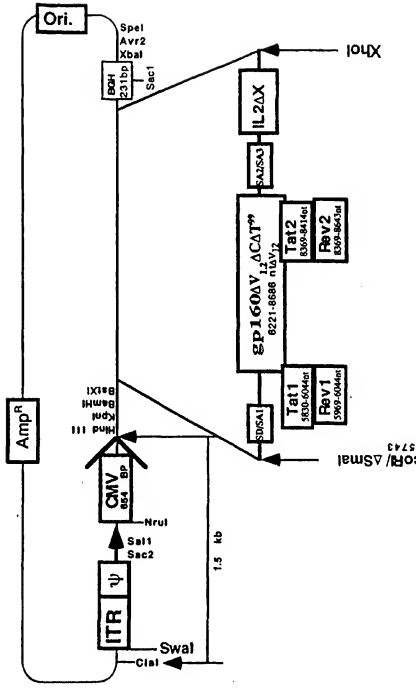


FIGURE 19A

pLAd-E^{m}ΔV$_{1,2}$ΔCΔT.TR-IL2

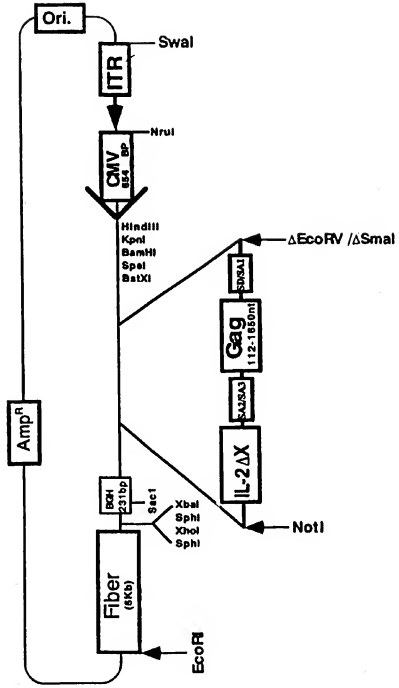
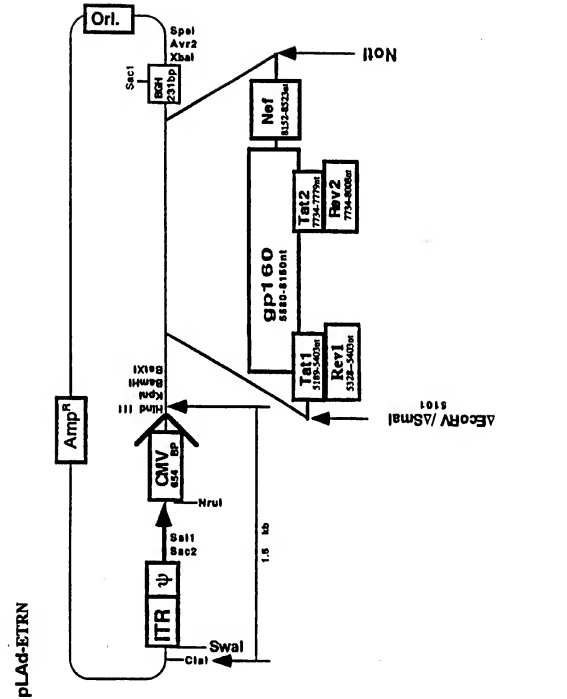


FIGURE 19B

pRAd.ORF6-G.IL2

FIGURE 20


pLAd-ETRN
Orl.
SpeI
Avr2
XbaI
Sac1
BGH
231bp
NotI
Nef
8132-8523nt
Tat2
7774-7779nt
Rev2
7734-8008nt
gp160
5880-8160nt
Tat1
5186-5403nt
Rev1
5328-5403nt
ΔEcoRV /ΔSmaI
5101
HindIII
KpnI
BamHI
SalXI
Amp^R
CMV
654 BP
NruI
Sal1
Sac2
Ψ
ITR
SwaI
ClaI
1.5 kb

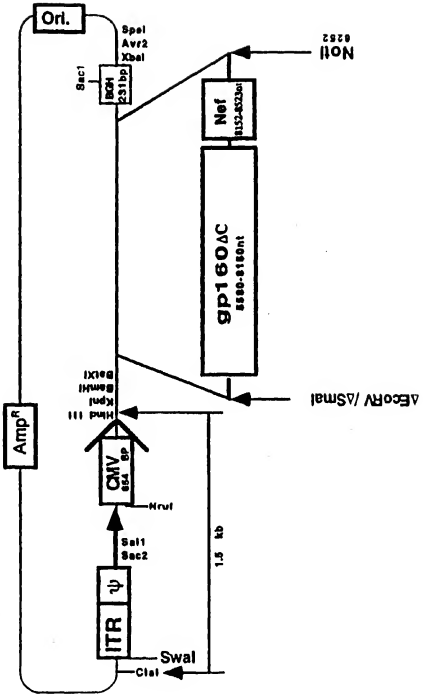


FIGURE 21

pLAd-E^{III}ΔC.N

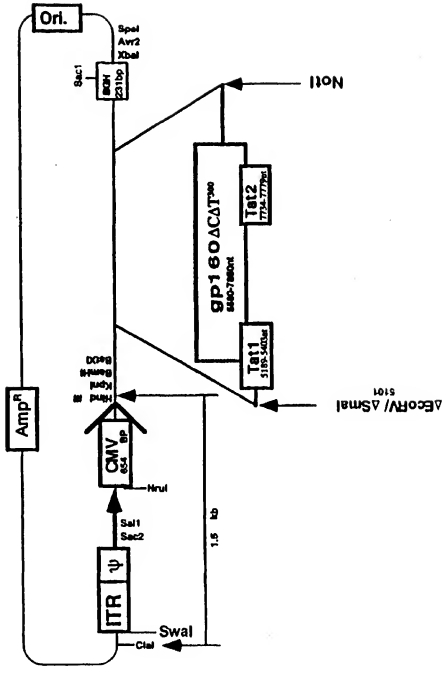


FIGURE 22

pLAd-E⁻ΔCΔT³⁰⁰.T

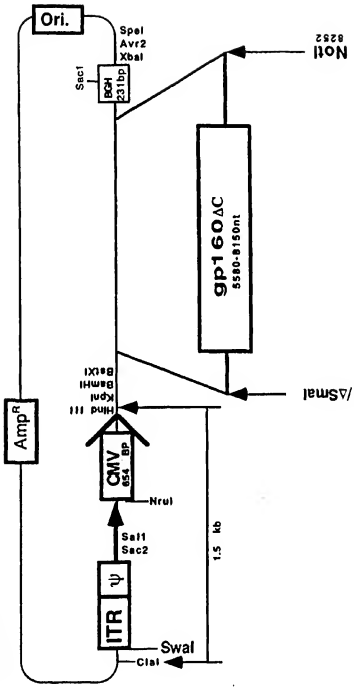


FIGURE 23A

pLAd-E$^{m}\Delta C$

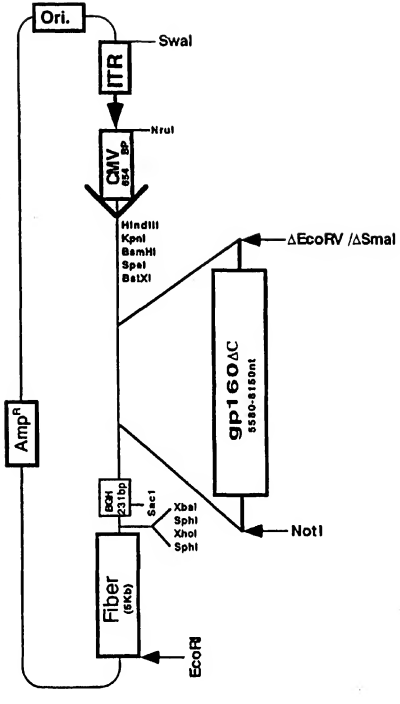


FIGURE 23B

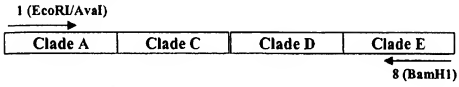
pRAd.ORF6-E^{III}ΔC

FIGURE 24

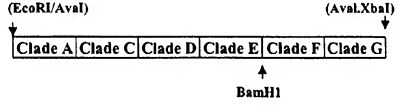
Step 1. Amplification of each individual clade A-G
1 (EcoR I/Ava I)
Clade A
2
3
Clade C
4
5
Clade D
6
7
Clade E
8 (BamH1)
9 (BamH1)
Clade F
10
11 (EcoR I/Ava I)
Clade G
12 (AvaI/XbaI)
Step 2. Amplification of every two clades AC, DE, FG
1 (EcoR I/Ava I)
Clade A
Clade C
4
5
Clade D
Clade E
8 (BamH1)
9 (BamH1)
Clade F
Clade G
12 (AvaI/XbaI)

FIGURE 24-cont.

Step 3. Amplification of clades ACDE



Step 4. Cloning the multi-clades into pSP73 vector



Step 5. Generation of duplicated multi-clades

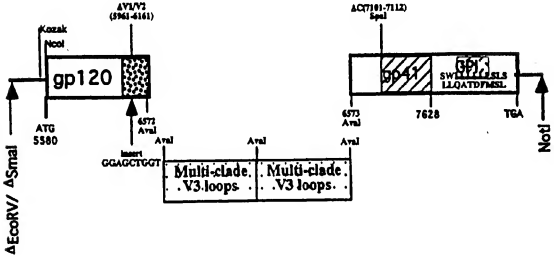
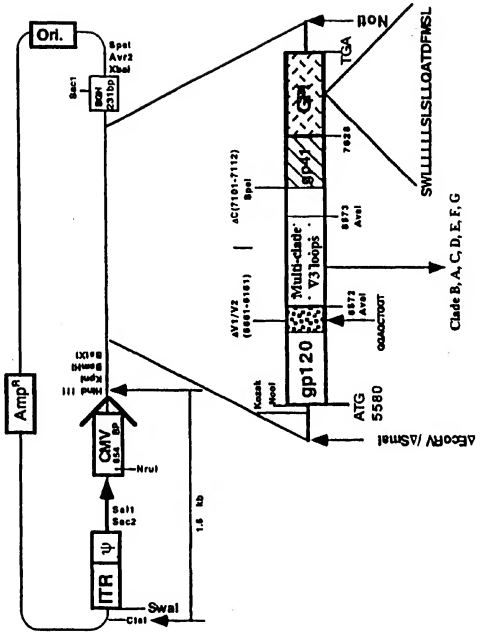


FIGURE 25



pLAd-E^m.V3

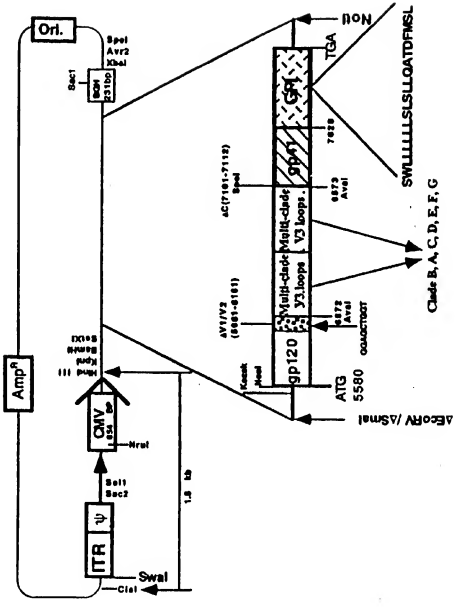
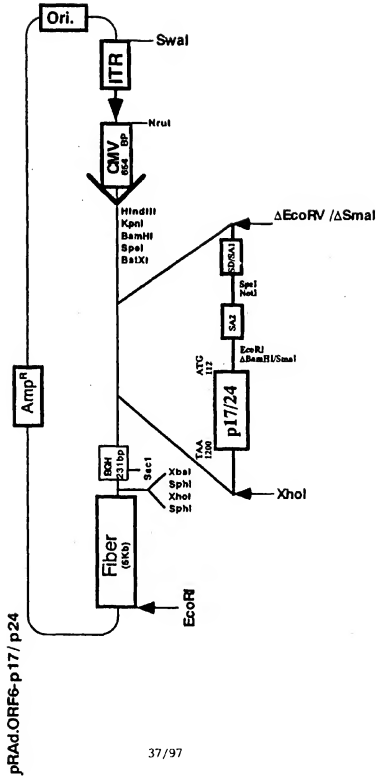

Ori.
Amp^R
CMV
ITR
Ψ
SwaI
ClaI
NruI
1.8 kb
TGA
gp41
gp120
ATG
5580
Clade B, A, C, D, E, F, G
SWLLLLLLSLSLLQATDFMSL
ΔEcoRV /ΔSmaI

FIGURE 26

FIGURE 27A


Ori.
SwaI
ITR
NruI
CMV
654 BP
HindIII
KpnI
BamHI
SpeI
BstXI
ΔEcoRV /ΔSmaI
SD/SA1
SpeI
NotI
SA2
EcoRI
ΔBamHI/SmaI
ATG
112
p17/24
TAA
1200
XhoI
AmpR
pIX
2131bp
SacI
XbaI
SphI
XhoI
SphI
Fiber
(6Kb)
EcoRI
pRAd.ORF6-p17/ p24

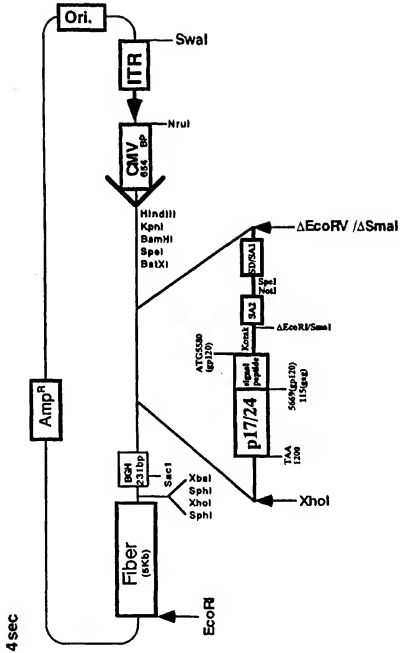


FIGURE 27B

pRAd.ORF6-p17/24sec

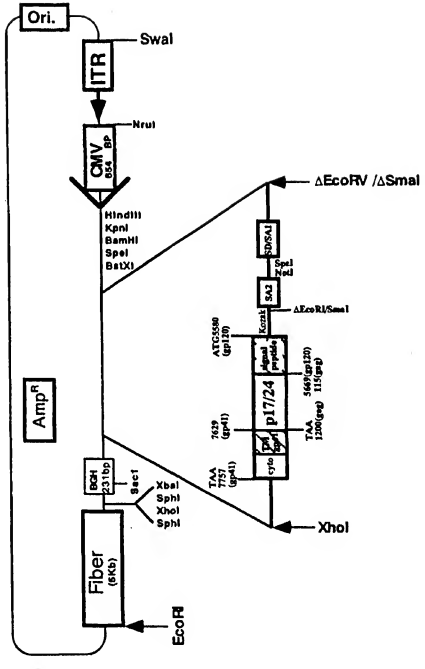


FIGURE 27C

RAd.ORF6-p17/24MB

FIGURE 28A

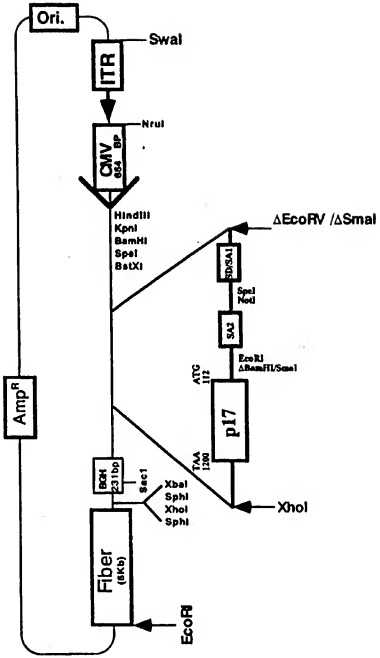
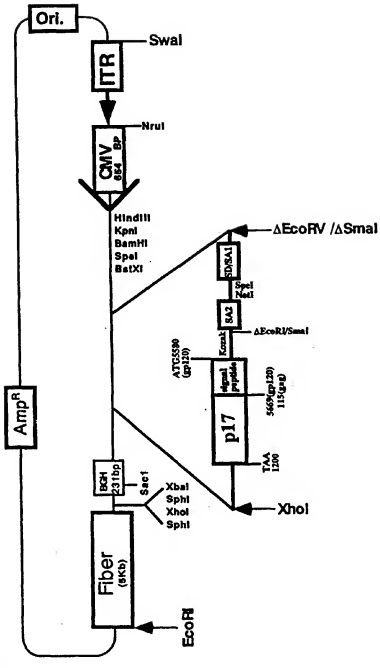
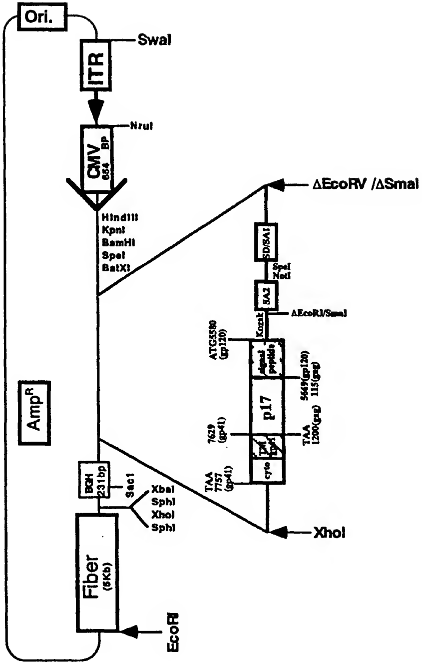

Ori.
SwaI
ITR
NruI
CMV
654 BP
HindIII
KpnI
BamHI
SpeI
BstXI
ΔEcoRV /ΔSmaI
SDSA1
SpeI
NotI
SA2
EcoRI
ΔBamHI/SmaI
ATG
172
p17
TAA
1200
AmpR
BGH
231bp
Sac1
XbaI
SphI
XhoI
SphI
XhoI
Fiber
(6Kb)
EcoRI
pRAd.ORF6-p17

FIGURE 28B



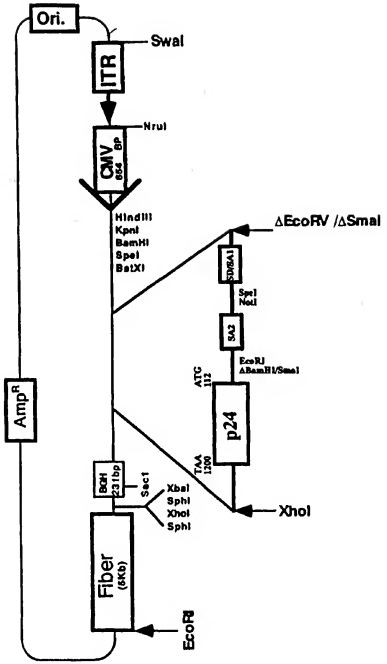
pRAd.ORF6- p17 sec

FIGURE 28C



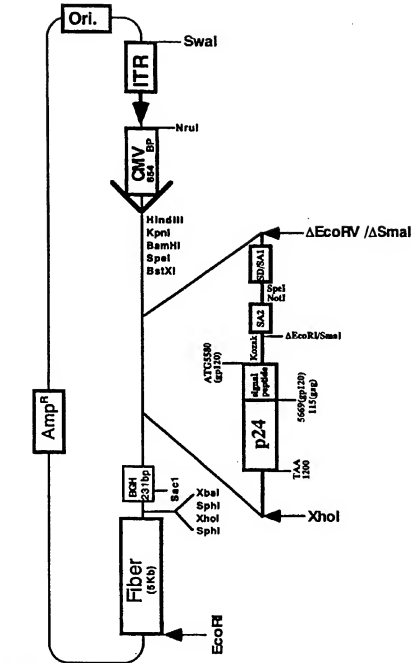
pRAd.ORF6-p17MB

FIGURE 29A



pRAd.ORF6-p24

FIGURE 29B


Ori.
SwaI
ITR
NruI
CMV
IE-1
HindIII
KpnI
BamHI
SpeI
BstXI
ΔEcoRV /ΔSmaI
SD/SA1
SpeI
NotI
SA2
ΔEcoRI/SmaI
KozAc
ATG(5'590 (gp120)
signal peptide
p24
5669(gp120) 115(gag)
TAA 1300
AmpR
BGH
231bp
SacI
XbaI
SphI
XhoI
SphI
XhoI
Fiber (5Kb)
EcoRI
pRAd.ORF6-p24 sec

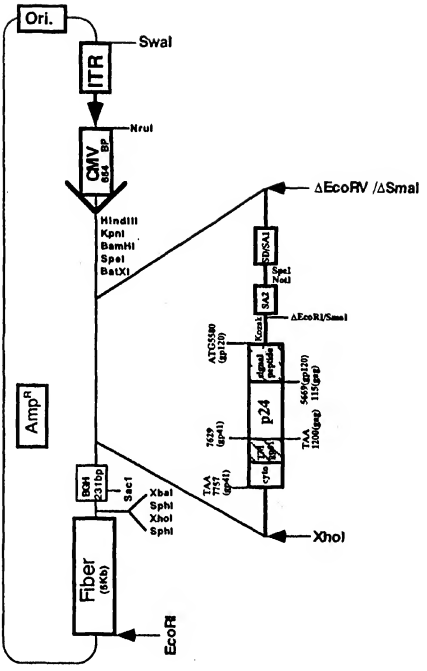


FIGURE 29C

pRAd.ORF6-p24MB

FIGURE 30A

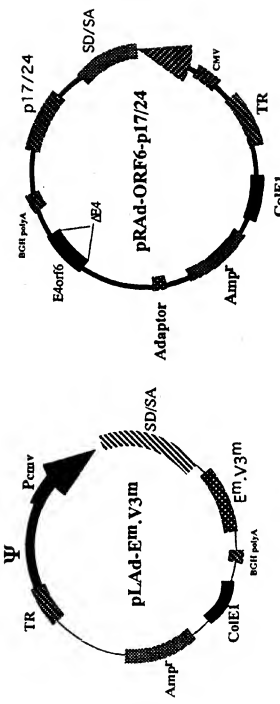

pRAd-ORF6-p17/24
p17/24
SD/SA
CMV
TR
ColE1
Ampr
Adaptor
E4orf6
ΔE4
BGH polyA
pLAd-Em.V3m
Ψ
TR
Pcmv
SD/SA
Em.V3m
BGH polyA
ColE1
Ampr

FIGURE 30B

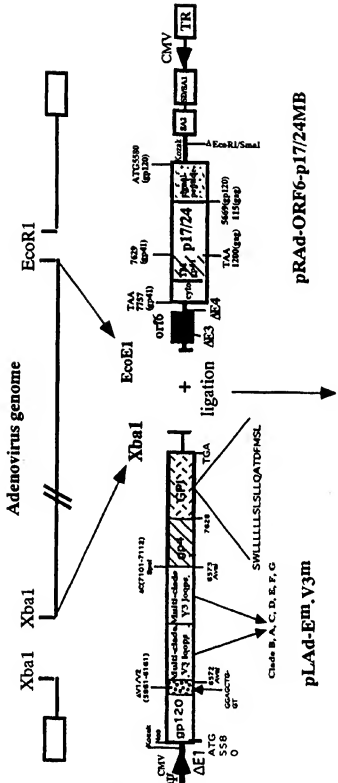

Adenovirus genome
Xba1
Xba1
EcoR1
EcoE1
Xba1
+
ligation
pLAd-E^{III}.V3^{III}
pRAd-ORF6-p17/24MB
CMV
TR
ΔE1
gp120
ΔE3
ΔE4
orf6
p17/24
EcoR1/SmaI
Clade B, A, C, D, E, F, G
SWLLLLLLSLLQATDFMSL

FIGURE 30B-continued

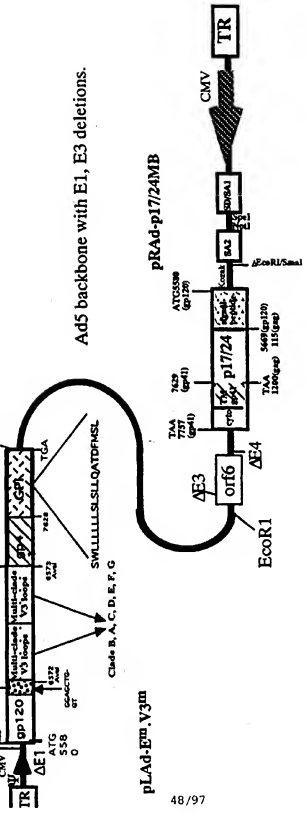


FIGURE 31A

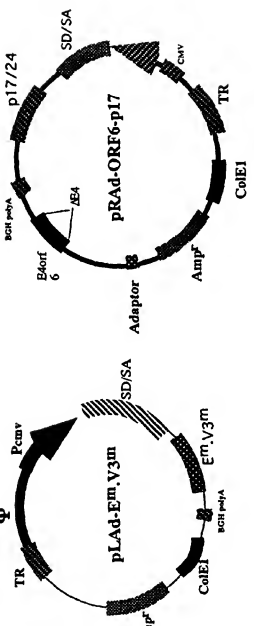

pRAd-ORF6-p17
p17/24
SD/SA
CMV
TR
ColE1
Ampr
Adaptor
βorf 6
ΔE4
BGH polyA
pLAd-Em.V3m
Ψ
TR
Pcmv
SD/SA
Em.V3m
BGH polyA
ColE1
Ampr

FIGURE 31B

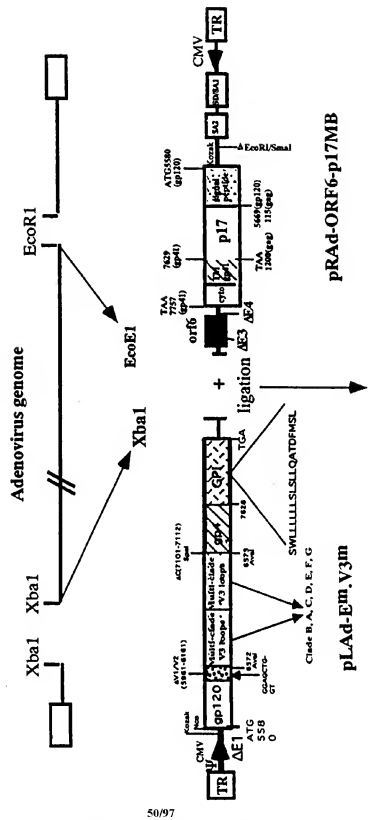
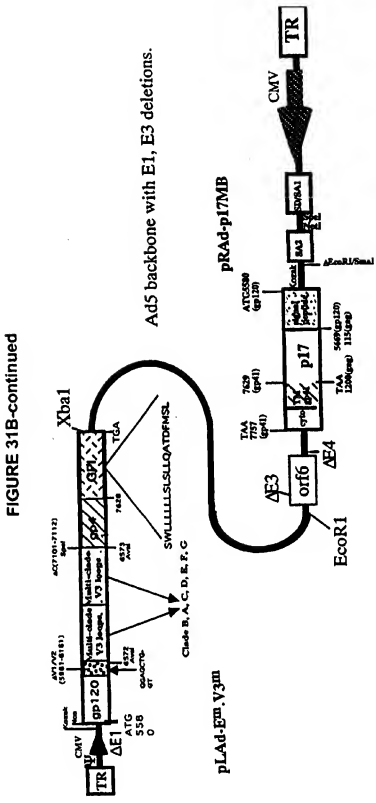

Adenovirus genome
EcoR1
EcoE1
Xba1
Xba1
Xba1
pLAd-E1m.V3m
pRAd-ORF6-p17MB
ligation
+
CMV
TR
ΔE1
gp120
Multi-clade V3 loops
Clade B, A, C, D, E, F, G
SWLLLLLLSLSLLQATDFMSL
ΔE3
ΔE4
orf6
p17
EcoRI/SmaI

FIGURE 31B-continued



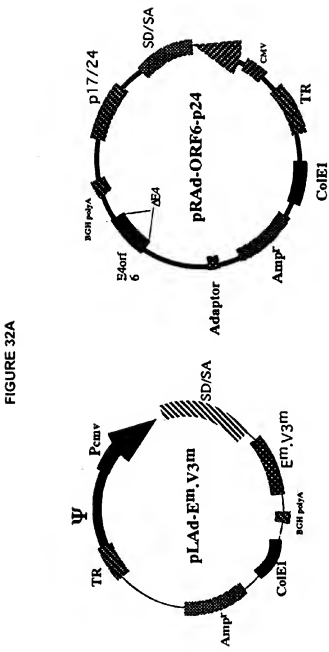

pRAd-ORF6-p24
p17/24
SD/SA
CMV
TR
ColE1
Ampr
Adaptor
ΔE4
BGH poly A
E4orf 6
pLAd-Em.V3m
Ψ
Pcmv
TR
Ampr
ColE1
BGH poly A
Em.V3m
SD/SA

FIGURE 32A

FIGURE 32B

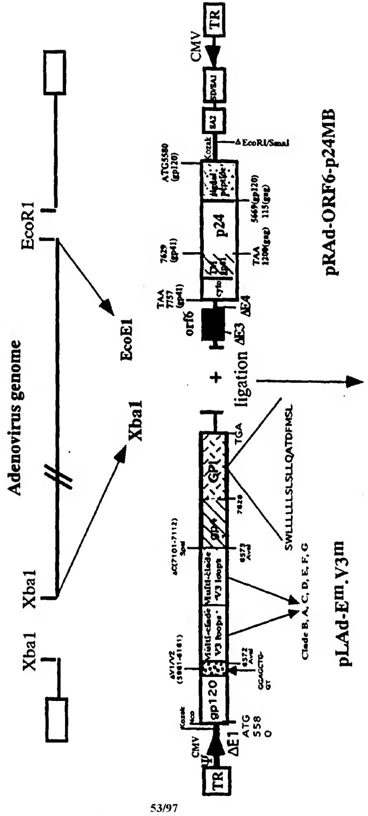

Adenovirus genome
Xba1
Xba1
EcoR1
Xba1
EcoE1
TR
CMV
ΔE1
gp120
Multi-clade V3 loops
Multi-clade V3 loops
gp41
GPI
TGA
SWLLLLLSLLLQATDFMSL
Clade B, A, C, D, E, F, G
pLAd-Em.V3m
+
ligation
orf6
ΔE3
ΔE4
cyto
p24
Kozak
SA2
SD/SA1
CMV
TR
ΔEcoRI/SmaI
pRAd-ORF6-p24MB

FIGURE 32B-continued

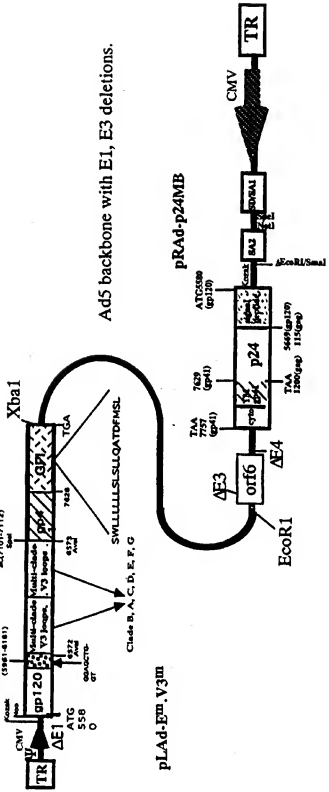


FIGURE 33

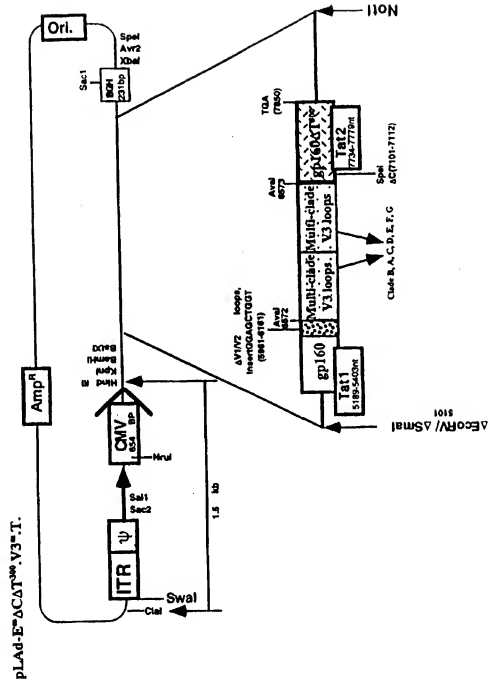
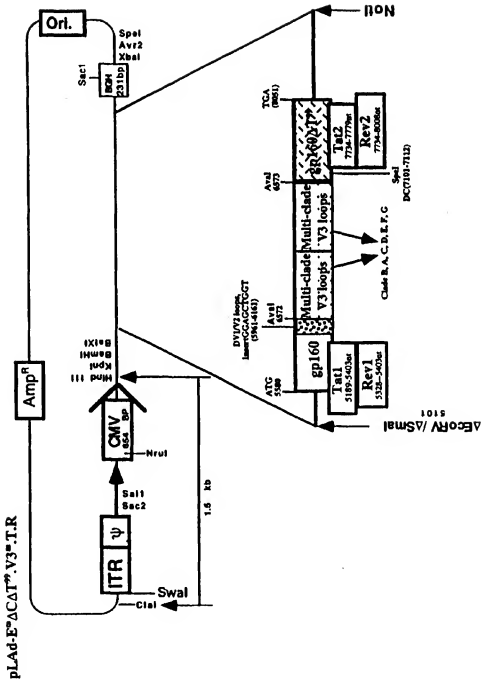

pLAd-E⁻ΔCΔ1ᵀᴿᵂ.V3⁻T.
Ori.
SpeI
Avr2
XbaI
Sac1
RSV
231bp
ITR
ψ
Sal1
Sac2
CMV
654 bp
MruI
AmpR
SwaI
ClaI
1.5 kb
gp160
Multi-clade
V3 loops
Multi-clade
V3 loops
Clade B, A, C, D, E, F, G
gp160ΔTM
Tat2
7734-7779nt
Tat1
5189-5403nt
TGA
(7840)
AvrII
6977
SpeI
Δ(7101-7112)
ΔV1/V2
loops,
InsertGGAGCTGGT
(6981-6161)
AvrII
6872
NotI
ΔEcoRV/ΔSmaI
5101

FIGURE 34


pLAd-E⁻ΔCΔT⁻.V3⁺T.R
ITR
ψ
SalI
Sac2
NruI
CMV
SwaI
ClaI
1.6 kb
Amp^R
Ori.
SpeI
AvrII
XbaI
Sac1
RRE
231bp
NotI
ΔEcoRV /ΔSmaI
5101
gp160
Tat1
5169-5405nt
Rev1
5328-5405nt
ATG
5188
Multi-clade V3 loops
Multi-clade V3 loops
Clade B, A, C, D, E, F, G
Tat2
7734-8379nt
Rev2
7734-8308nt
TCA
(8611)
AvrII
6577
SpeI
DCT(7101-7112)

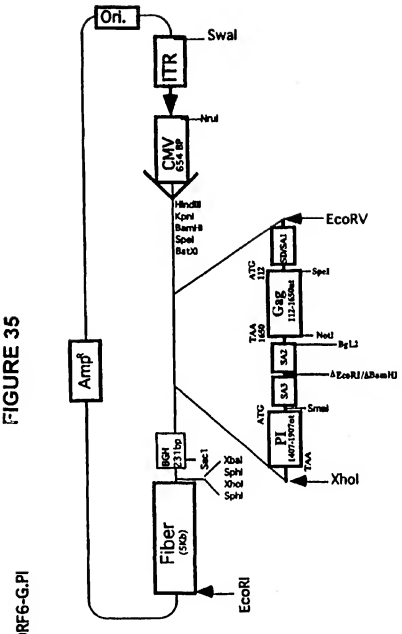

Ori.
SwaI
ITR
NruI
CMV
654 bp
HindIII
KpnI
BamHI
SpeI
BstXI
EcoRV
ATG
112
Gag
112-1656nt
SpeI
TAA
1656
NotI
BglII
SA2
SA3
ΔEcoRI/ΔBamHI
ATG
SmaI
P1
1497-1597nt
TAA
XhoI
Amp
BGH
231bp
SacI
XbaI
SphI
XhoI
SphI
Fiber
(3kb)
EcoRI
pRAd.ORF6-G.PI

FIGURE 35

FIGURE 36

pRAd.ORF6-G-PI

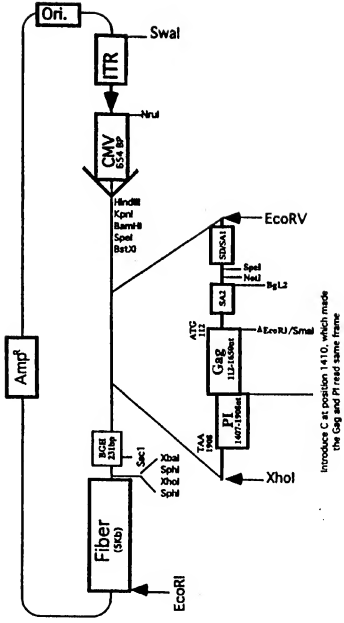


FIGURE 37

SD/SA1.2.3 vector

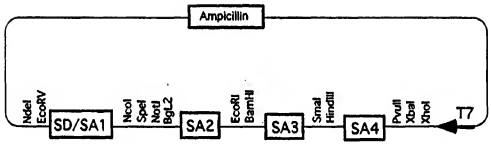


FIGURE 38

DNA Sequence of Env/Tat/Rev from BH10 clone [SEQ ID NO: 14]:

Gaattctgcaacaactgctgtttatccatttt**cagaattggg**tgtcgacat
EcoRI

agcagaatagggcttactcgacagaggagagcaagaaatggagccagtagatcctagactagagccccggga
agcatccaggaagtcagcctaaaactgcttgtaccaattgctattgtaaaaagtgttgcttt**ca**ttgccaa
gtttgtttcataacaaaagccttaggcatctcctatggcaggaagaagcggagacagcgacgaagacccccc
tcaaggcagtcagactcatcaagtttctctatcaaagcagtaagtagtacatgtaatgcaacctataccaaa
tagcaatagtagcattagtagtagcaataatagcaatagttgtgtggtccatagtaatcatagaatat
aggaaaatattaagacaaagaaaaatagacaggttaattgatagactaatagaaagagcagaagacagtgg
caatgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatggggcaccatgctccttggg
atgttgatgatctgtagtgctacagaaaaattgtgggtcacagtctattatggggtacctgtgtggaagga
agcaaccaccactctatttttgtgcatcagatgctaaagcatatgatacagaggtacataatgttgggcca
cacatgcctgtgtacccacagaccccaacccacaagaagtagtattggtaaatgtgacagaaaatttttaac
atgtggaaaaatgacatggtagaacagatgcatgaggatataatcagttttatgggatcaaagcctaaagcc
atgtgtaaaattaaccccactctgtgttagtttaaagtgcactgatttgaagaatgatactaatacccaata
gtagtagcgggagaatgataatggagaaaggagagataaaaaactgctctttcaatatcagcacaagcata
agaggtaaggtgcagaaagaatatgcatttttttataaacttgatataatacccaatagatgatgatactac
cagctatacgttgacaagttgtaacacctcagtcattacacaggcctgtccaaaggtatcctttgagccaa
ttcccatacattattgtgcccgggctggttttgcgattctaaaatgtaataataagacgttcaatggaaca
ggaccatgtacaaatgtcagcacagtacaatgtacacatggaattaggccagtagtatcaactcaactgct
gttaaatggcagtctggcagaagaagaggtagtaattagatctgccaattccacagacaatgctaaaacca
taatagtacagctgaacaatctgtagaaattaattgtacaagacccaacaacagcaatacaagaaaaagtatc
cgtatccagaggaccagggagagcatttgttacaatagggaaaattaggaaatatgagacaacgcacattg
taacattagtagagcaaaatggaataacacttaaaacagatagatagcaaattaagagaacaatttggaa
ataataaacaatcaatcttttaagcagtcctcaggagggacccagaaattgtaacgcagcagtttaattgt
ggaggggaatttttctactgtaattcaacacaactgttaatagtacttggtttaatagtacttggagta
ctaaagggtcaaataacactgaaggaagtgacacaatcacctcccatgcagaataaaacaaattataaac
atgtggcaggaagtaggaaaagcaatgtatgcccctcccatcagtggacaaattagatgttcatcaaatat
tacaggggctgctattaacaagagatggtggtaatagcaacaatgagtccgagatcttcagacctggaggag
gagatatgagggacaattggagaagtgaattatataaatataaagtagtaaaaattgaaccattaggagta
gcacccaccaaggcaaagagaagagtggtgcagagagaaaaagagcagtgggaatagggagcttttgttcct
tgggttcttgggagcagcaggaagcactatgggcgcagcgtcaatgacgctgacggtacaggccagacaat
tattgtctggtatagtgcagcagcagaacaatttgctgagggctattgaggcgcaacagcatctgttgcaa
ctcacagtctgggcatcaagcagctccaggcaagaatcctggctgtggaaagatacctaaaggatcaaca
gctcctggggattggggttgctctggaaaactcatttgcaccactgctgtgccttggaatgctagttgga
gtaataaatctctggaacagatttggaatcactacgtcggatggagtgggacagagaaattaacaattac
acaagcttaatacactccttaattgaagaatcgcaaaaccagcaagaaaagaatgaacaagaattattgga
attagataaatgggcaagtttgtggaattggtttaacataacaaattggctgtggtatataaaattattca
taatgatagtaggaggcttggtaggtttaagaatagtttttgctgtactttctgtagtgaatagagttagg
cagggatattcaccattatcgtttcagacccacctcccaatcccgaggggacccgacaggcccgaaggaat
agaagaagaaggtggagagagagacagagacagatccattcgattagtgaacggatcctagcactttatct
gggacgatctgcggagcctgtgcctctttcagctacccaccgcttgagagacttactcttgattgtaacgagg
attgtggaaccttctgggacgcaggggtgggaagccctcaaatattggtggaatctcctacagtattggag
tcaggagctaaagaatagtgctgttagcttgctcaatgccacagctatagcagtagctgaggggacagata
gggttatagaagtagtacaaggagcttatagagctattcgccacatacctagaagaataagacagggcttg
gaaaggatttgctatagatgggtggcaagtggtcaaaaagtagtgtggttggatggcctgctgtaaggg
aaagaatgagacgagctgagccagcagcagatggggtgggagcagcatctcgag
XhoI

FIGURE 39

DNA Sequence of IL-2ΔX [SEQ ID NO: 15]:

Tcactctctttaatcactactcacagtaacctcaactcctgccacaatgta
caggatgcaactcctgtcttgcattgcactaagtcttgcacttgtcacaaa
cagtgcacctacttcaagttctacaaagaaaacacagctacaactggagca
tttactgctggatttacagatgattttgaatggaattaataattacaagaa
tcccaaactcaccaggatgctcacatttaagttttacatgcccaagaaggc
cacagaactgaaacatcttcagtgtcttgaagaagaactcaaaccctctgga
ΔXbaI (cta → ctt)
ggaagtgctaaatttagctcaaagcaaaaactttcacttaagacccaggga
cttaatcagcaatatcaacgtaatagttctggaactaaagggatctgaaac
aacattcatgtgtgaatatgctgatgagacagcaaccattgtagaatttct
gaacagatggattacctttttgtcaaagcatcatctcaacactaacttga

FIGURE 40

DNA Sequence of $Env^{m}\Delta C\Delta T^{300}$ (HIV strain BH10) [SEQ ID NO: 16]:

Gaattcgccaccatgggagtcaaggagaaatatcagcacttgtggagatg
EcoRI Kozak NcoI
ggggtggagatggggcaccatgctccttgggatgttgatgatctgtagtgctacagaaaaa
ttgtgggtcacagtctattatggggtacctgtgtggaaggaagcaaccaccactctatttt
gtgcatcagatgctaaagcatatgatacagaggtacataatgtttgggccacacatgcctg
tgtacccacagaccccaacccacaagaagtagtattggtaaatgtgacagaaaattttaac
atgtggaaaaatgacatggtagaacagatgcatgaggatataatcagtttatgggatcaaa
gcctaaagccatgtgtaaaattaaccccactctgtgttagtttaaagtgcactgatttgaa
gaatgatactaataccaatagtagtagcgggagaatgataatggagaaaggagagataaaa
aactgctctttcaatatcagcacaagcataagaggtaaggtgcagaaagaatatgcatttt
tttataaacttgatataatacccaatagatatgatactaccagctatacgttgacaagttg
taacacctcagtcattacacaggcctgtccaaaggtatcctttgagccaattcccatacat
tattgtgccccggctggtttgcgattctaaaatgtaatataagacgttcaatggaacag
gaccatgtacaaatgtcagcacagtacaatgtacacatggaattaggccagtagtatcaac
tcaactgctgttaaatggcagtctggcagaagaagaggtagtaattagatctgccaatttc
acagacaatgctaaaacccatataatagtacagctgaaccaatctgtagaaattaattgtacaa
gacccaacaacaatacaagaaaaagtatccgtatccagagaggaccagggagagcatttgt
tacaatagggaaaaatagggaaatatgagacaagcacattgtaacattagtagagcaaaatgg
aataacactttaaaacagatagatagcaaattaagagaacaatttggaaataataaaacaa
taatctttaagcagtcctcaggaggggacccagaaattgtaacgcacagttttaattgtgg
aggggaatttttctactgtaattcaacacaactgttaatagtacttggtttaatagtact
tggagtactaaagggtcaaataacactgaaggaagtgacacaatcacctcccatgcagaa
taaaacaaattataaacatgtggcaggaagtaggaaaagcaatgtatgcccctcccatcag
tggacaaattagatgttcatcaaatattacagggctgctattaacaagagatggtggtaat
agcaacaatgagtccgagatcttcagacctggaggaggagatatgagggacaattggagaa
gtgaattatataaatataaagtagtaaaaattgaaccattaggagtagcacccaccaaggc
aaagagaagagtggtgcagACTAGTgcagtgggaataggagctt
ΔCleavage site(agagaaaaaaga)→SpeI
tgttccttgggttcttgggagcagcaggaagcactatgggcgcagcgtcaatgacgctgac
ggtacaggccagacaattattgtctggtatagtgcagcagcagaacaatttgctgagggct
attgaggcgcaacagcatctgttgcaactcacagtctggggcatcaagcagctccaggcaa
gaatcctggctgtggaaagatacctaaaggatcaacagctcctggggatttggggttgctc
tggaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaataaatctctg
gaacagatttggaatcacatgacctggatggagtgggacagagaaattaacaattacacaa
gcttaatacactccttaattgaagaatcgcaaaaccagcaagaaaagaatgaacaagaatt
attggaattagataaatgggcaagtttgtggaattggttaacataacaaattggctgtgg
tatataaaattattcataatgatagtaggaggcttggtaggtttaagaatagtttttgctg
tactttctgtagtgaatagagttaggcagggatattcaccattatcgtttcagacccacct
cccaatcccgaggggacccgacaggcccgaaggaatagaagaagaaggtggagagagagac
agagacagatccattcgattagtgaacggatccttagcacttatctggtaa

FIGURE 41A

DNA Sequence of Full length HIV-1 Gag [SEQ ID NO: 17]:

ggctagaaggagagaggatgggtgcgagagcgtcagtattaagcgggggag
aattagatcgatgggaaaaaattcggttaaggccagggggaaagaaaaaat
ataaattaaaacatatagtatgggcaagcagggagctagaacgactacaac
catcccttcagacaggatcagaagaacttagatcattatataatacagtag
caaccctctattgtgtgcatcaaaggatagagataaaagacaccaaggaag
ctttagacaagatagaggaagagcaaaacaaaagtaagaaaaaagcacagc
aagcagcagctgacacaggacacagcagtcaggtcagccaaaattacccta
tagtgcagaacatccaggggcaaatggtacatcaggccatatcacctagaa
ctttaaatgcatgggtaaaagtagtagaagagaaggctttcagcccagaag
taataccccatgttttcagcattatcagaaggagccaccccacaagatttaa
acaccatgctaaacacagtgggggacatcaagcagccatgcaaatgttaa
aagagaccatcaatgaggaagctgcagaatgggatagagtacatccagtgc
atgcagggcctattgcaccaggccagatgagagaaccaaggggaagtgaca
tagcaggaactactagtacccttcaggaacaaatagggatggatgacaaata
atccacctatcccagtaggagaaatttataaaagatggataatcctgggat
taaataaaatagtaagaatgtatagccctaccagcattctggacataagac
aaggaccaaaagaacccttttagagactatgtagaccggttctataaaactc
taagagccgagcaagcttcacaggaggtaaaaaattggatgacagaaacct
tgttggtccaaaatgcgaacccagattgtaagactattttaaaagcattgg
gaccagcggctacactagaagaaatgatgacagcatgtcagggagtaggag
gacccggccataaggcaagagttttggctgaagcaatgagccaagtaacaa
atacagctaccataatgatgcagagaggcaattttaggaaccaaagaaaga
tggttaagtgtttcaattgtggcaaagaagggcacacagccagaaattgca
gggcccctaggaaaaagggctgttggaaatgtggaaaggaaggacaccaaa
tgaaagattgtactgagagacaggctaatttttttagggaagatctggcctt
cctacaagggaaggccagggaattttcttcagagcagaccagagccaacag
ccccaccatttcttcagagcagaccagagccaacagccccaccagaagaga
gcttcaggtctggggtagagacaacaactccccctcagaagcaggagccga
tagacaaggaactgtatcctttaacttccctcagatcactctttggcaacg
acccctcgtcacaataa

FIGURE 41B

Amino Acid Sequence of HIV-1 (Strain BH10) Gag (SEQ ID NO: 18):

M	G	A	R	A	S	V	L	S	G	G	E	L	D	R	W	E	K
I	R	L	R	P	G	G	K	K	K	Y	K	L	K	H	I	V	W
A	S	R	E	L	E	R	L	Q	P	S	L	Q	T	G	S	E	E
L	R	S	L	Y	N	T	V	A	T	L	Y	C	V	H	Q	R	:
E	I	K	D	T	K	E	A	L	D	K	I	E	E	E	Q	N	K
S	K	K	K	A	Q	Q	A	A	K	D	T	G	H	S	S	Q	V
S	Q	N	Y	P	I	V	Q	N	A	Q	G	Q	M	V	H	Q	A
I	S	P	R	T	L	N	A	W	V	K	V	Q	E	A	K	A	F
S	P	E	V	I	P	M	F	S	A	L	S	E	G	A	T	P	Q
D	L	N	T	M	L	N	T	V	G	G	H	Q	D	A	M	Q	M
L	K	E	P	I	N	E	E	A	A	E	W	D	P	A	H	P	V
H	A	G	T	S	A	P	G	Q	M	R	D	Q	R	R	S	D	I
A	G	I	P	G	T	L	Q	E	Q	I	E	I	P	M	N	N	P
P	I	V	R	Y	P	I	Y	K	R	W	G	I	I	L	L	P	K
I	V	P	F	D	M	P	P	S	I	L	L	D	I	R	G	E	K
E	P	S	Q	V	R	V	I	R	F	Y	Y	K	T	L	A	N	Q
A	S	P	D	K	E	N	Q	M	T	E	T	T	G	L	A	L	A
N	P	M	M	A	C	I	G	K	A	L	A	G	P	A	H	R	E
E	M	A	E	M	T	S	L	V	G	G	G	N	A	P	I	Q	V
L	A	N	F	N	A	Q	G	T	V	K	T	V	G	G	N	K	R
G	N	H	T	R	R	M	V	K	T	M	K	V	K	K	M	K	E
G	H	K	E	A	C	N	P	R	A	A	R	M	R	R	C	K	C
G	K	E	I	G	T	R	A	K	D	D	C	P	N	K	G	K	L
P	E	E	P	W	S	Q	P	K	G	G	T	R	P	R	W	Q	R
P	P	P	E	T	D	S	Y	F	L	L	P	Q	E	E	N	T	P
E	E	P	I	S	S	P	R	G	V	E	S	E	L	P	P	Q	Q
N	D	P	S	K	S	E	Q	Y	P	L	T	R	T	L	S	L	G

FIGURE 42

DNA Sequence of $E^{m}\Delta C\Delta T^{99}$.T.R (HIV strain pNL4-3) [SEQ ID NO: 19]:

Gaattctgcaacaactgctgtttatccatttcagaattgggtgtcgacatag
EcoRI
cagaatagggcgttactcgacagaggagagcaagaaatggagccagtagatcctagactagagcccctggaagca
tccaggaagtcagcctaaaactgcttgtaccaattgctattgtaaaaagtgttgctttcattgccaagtttgt
ttcatgacaaaagccttaggcatctcctatggcaggaagaagcggagacagcgacgaagagctcatcagaaca
gtcagactcatcaagcttctctcatcaaagcagtaagtagtacatgtaatgcaacctataatagtagcaatagt
agcattagtagtagcaattataatagcaatagttgtgtggtccatagtaatcatagaatatagggaaaatatta
agacaaagaaaaatagacaggttaattgatagactaatagaaagagcagaagacagtggcaatgagagtgaag
gagaagtatcagcacttgtggagatgggggtggaaatggggcaccatgctccttgggatattgatgatctgta
gtgctacagaaaaattgtgggtcacagtctattatggggtacctgtgtggaaggaagcaaccaccactctatt
ttgtgcatcagatgctaaagcatatgatacagaggtacatatgtttgggccacacatgccctgtgtacccaca
gaccccaacccacaagaagtagtattggtaaatgtgacagaaaatttaacatgtggaaaaatgacatggtag
aacagatgcatgaggatataatcagtttatgggatcaaagcctaaagccatgtgtaaaattaacccctcactct
tgttagtttaaagtgcactgatttgaagaatgatactaatacccaatagtagtagcgggagaatgataatggag
aaaggagagataaaaaactgctctttcaatatcagcacaagcataagagtaaggtcgacgaaagaatatgcat
tcttttataaacttgatatagtaccaatagataatacca
gctataggttgataagttgtaacacctcagtcattacacaggcctgtccaaaggtatcctttgagccaattcc
catacattattgtgccccggctggttttgcgattctaaaatgtaataataagacgttcaatggaacaggacca
tgtacaaatgtcagcacagtacaatgtacacatggaatcaggccagtagtatccaactcaactgctgttaaatg
gcagtctagcagaagaagatgtagtaattagatctgccaatttcacagacaatgctaaaacccataatagtaca
gctgaacacatcttgtagaaactaattgtacaagacccaacaacaatacaagaaaaagtatccgtatccagagg
ggaccaggggagagcattgttgtcacaatagggaaaaatggaaatatgagacaagcacattgtaacattaggag
caaaatggaatgccacttttaaaacagatagctagcaaatttaagagaaccaatttggaaataataaaacaataat
ctttaagcaatcctcaggaggggacccagaaattgtaacgcacagtttaattgtggaggggaatttttctac
tgtaattcaacacaactgtttaatagtacttggtttaatagtacttggagtactgaagggtcaaataacactg
aaggaagtgacacaatcacactccatgcagaataaaacaatttatataaacatgtggcaggaagtaggaaaagc
aatgtatgcccctcccatcagtggacaaattagatgttcatcaaatattactgggctgctattaacaagagat
ggtggtaataacaacaatgggtccgagatcttcagacctggaggaggcgatatgagggacaattggagaagtg
aattatataaatataaagtagtaaaaattgaaccattaggagtagcacccaccaaggcaaagagaagagtggt
gcagACTAGTgcagtgggaataggagctttgttccttg
ΔCleavage site(agagaaaaaaga)→SpeI
ggttcttgggagcagcaggaagcactatgggctgcacgtcaatgacgctgacggtacaggccagacaattatt
gtctgatatagtgcagcagcagaacaatttgctgagggctattgaggcgcaacagcatctgttgcaactcaca
gtctggggcatcaaacagctccaggcaagaatcctggctgtggaaagatacctaaagatcatcacaagtcctgg
ggatttgggggttgctctggaaaactcatttgcaccactgctgtccttggaatgctagttggagtaataaatc
tctggaacagatttggaatcacatgacctggatggagtgggacagagaaattaacaattacacaagctctaata
cactcctaattgaagaatcgcaaaaccagcaagaaagaatgaacaagaattattggaattagataaatgggg
caagtttgtggaattggtttaacataacaaattggctgtggtatataaaattattcataatgatagtaggagg
cttggtaggtttaagaatagtttttgctgtactttctatagtgaatagagttaggcagggatattcaccatta
tcgtttcagacccacctcccaatcccgaggggacccgacaggcccgaaggaatagaagaagaaggtggagaga
gagacagagacagatccattcgattagtgaacggatcctagcactttatctgggacgatctgcggagcctgtg
cctcttcagctaccaccgcttgagagacttactcttgattgtaacgaggattgtggaactttctgggacgcagg
gggtggggaagccctcaaatattggtggaatctcctacagtgtattggagtcaggaactaaagaatagtgctgtta
acttgctcaatgccacagccatagcagtagctgagtaa

FIGURE 43

DNA Sequence of $E^{n}\Delta V_{12}\Delta C\Delta T^{99}$.T.R (Strain pNL4-3) [SEQ ID NO: 20]:

Gaattctgcaacaactgctgtttatccatttcagaattgggtgtcgacatag
EcoRI

Cagaatagggcgttactcgacagaggagagcaagaaatggagccagtagatcctagactagagcccctggaagca
tccaggaagtcagcctaaaactgcttgtaccaattgctattgtaaaaagtgttgctttcattgccaagtttgt
ttcatgacaaaagccttaggcatctcctatggcaggaagaagcggagacagcgacgaagagctcatcagaaca
gtcagactcatcaagcttctctatcaaagcagtaagtagtacatgtaatgcaacctataaatagtagcaatagt
agcattagtagtagcaataataatagcaatagtttgtgtggtccatagtaatcatagaatatagggaaaatatta
agacaaagaaaaatagacaggttaattgatagactaatagaaagagcagaagacagtggcaatgagagtgaag
gagaagtatcagcacttgtggagatggggtggaaatggggcaccatgctccttgggatattgatgatctgta
gtgctacagaaaaattgtgggtcacagtctattatggggtacctgtgtggaaggaagcaaccaccactctatt
ttgtgcatcagatgctaaagcatatgatacagaggtacataatgtttgggccacacatgcctgttgtaccccaca
gaccccaccccacaagaagtagtattggtaaatgtgcagcaaaatttaacatgtggaaaaatgacatggtag
aacagatgcatgaggatataatcagtttatgggatcaaagcctaaagccatgtgtaaaattaacccccactctg
tgtt ΔV1 and V2 loops
Agttgtaacaccttcagtcattacacaggcctgtccaaaggtatcctttgagccaattcccatacattattgtg
ccccgcgctggttttgcgattctaaaatgtaataataagacgttcaatggaacagggaccatgtacaaatgtcag
cacagtacaatgtacacatggaatcaggccagtagtatcaactcaactgctgttaaatggcagtctagcagaa
gaagatgtagtaattagatctgccaatttcacagacaatgcactctaaaaccataatagtacagctgaacacatctg
tagaaattaattgtacaagacccaacaacaatacaagaaaaagtatccgtatccagaggggaccagggagagc
atttgttacaatagggaaaaatagggaaatatgagacaagcacattgtaacattagtagagcaaaatggaatgcc
actttaaaacagatagctagcaaattaagagaacaattgggaaataataaaacaataatcctttaagcaatcct
caggaggggacccagaaattgtaacgcacagttttaattgtggaggggaatttttctactgtaatttcaacaca
actgtttaatagtacttggtttaatagtacttggagtactgaagggtcaaataacactgaaggaagtgacaca
atcacactcccatgcagaatataaacaatttataaacatgtggcaggaagtaggaaaagcaatgtatgcccctc
ccatcagtggacaaattagatgttcatcaaatattactgggctgctattaacaagagatggtggtaataacaa
caatgggtccgagatcttcagacctggaggaggcgatatgagggacaattggagaagtgaattatataaatat
aaagtagtaaaaattgaaccattaggagtagcacccaccaaggcaaagagaagagtggtgcagAC TAGTgcag
tgggaataggagctttgttccttgggttcttgggagca
ΔCleavage site(agagaaaaaaga)→SpeI

gcaggaagcactatgggctgcacgtcaatgacgctgacggtacaggccagacaattattgtctgatatagtgc
agcagcagaacaatttgctgagggctattgaggcgcaacagcatcctgttgcaactcacagtctggggcatcaa
acagctccaggcaagaatcctggctgtggaaagatacctaaaggatcaacagctcctggggattttggggttgc
tctggaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaataaatctctggaacagatttt
ggaataacatgacctggatggagtgggacagagaaattaacaattacacaagcttaatacactccttaattga
agaatcgcaaaaccagcaagaaaagaatgaacaagaattattggaattagataaatgggcaagtttgtggaat
tggtttaacataacaaaattggctgtggtatataaaattattcataatgatagtaggaggcttggtaggtttaa
gaatagttttgctgtactttctatagtgaatagagttaggcagggatattcaccattatcgtttcagaccca
cctcccaatcccgaggggacccgacaggcccgaaggaatagaagaagaaggtggagagagagacagagacaga
tccattcgattagtgaacggatccttagcacttatctgggacgatctgcggagcctgtgcctcttcagctacc
accgcttgagagacttactcttgattgtaacgaggattgtggaacttctgggacgcagggggtgggaagccct
caaatattggtggaatctcctacagtattggagtcaggaactaaagaatagtgctgttaacttgctcaatgcc
acagccatagcagtagctgagtaa

FIGURE 44

DNA Sequence of Env^{m}ΔC.T.R.N (Strain BH10) [SEQ ID NO: 21]:

Gaattctgcaacaactgctgtttatccatttcagaattgggtgtcgacat
EcoRI
agcagaataggcgttactcgacagaggagagcaagaaatggagccagtagatcctagactagagccctgga
agcatccaggaagtcagcctaaaactgcttgtaccaattgctattgtaaaaagtgttgctttcattgccaa
gtttgtttcataacaaaagccttaggcatctcctatggcaggaagaagcggagacagcgacgaagacctcc
tcaaggcagtcagactcatcaagtttctctatcaaagcagtaagtagtacatgtaatgcaacctatacaaa
tagcaatagtagcattagtagtagcaataataatagcaatagttgtgtggtccatagtaatcatagaatat
aggaaaatattaagacaaagaaaaatagacaggttaattgatagactaatagaaagagcagaagacagtgg
caatgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatggggcaccatgctccttggg
atgttgatgatctgtagtgctacagaaaaattgtgggtcacagtctattatggggtacctgtgtggaagga
agcaaccaccactctattttgtgcatcagatgctaaagcatatgatacagaggtacataatgtttgggcca
cacatgcctgtgtacccacagaccccaacccacaagaagtagtattggtaaatgtgacagaaaattttaac
atgtggaaaaatgacatggtagaacagatgcatgaggatataatcagtttatgggatcaaagcctaaagcc
atgtgtaaaattaaccccactctgtgttagtttaaagtgcactgatttgaagaatgatactaataccaata
gtagtagcgggagaatgataatggagaaaggagagataaaaaactgctctttcaatatcagcacaagcata
agaggtaaggtgcagaaagaatatgcatttttttataaacttgatataataccaatagataatgatactac
cagctatacgttgacaagttgtaacacctcagtcattacacaggcctgtccaaaggtatcctttgagccaa
ttcccatacattattgtgccccggctggttttgcgattctaaaatgtaataataagacgttcaatggaaca
ggaccatgtacaaatgtcagcacagtacaatgtacacatggaattaggccagtagtatcaactcaactgct
gttaaatggcagtctggcagaagaagaggtagtaattagatctgccaatttcacagacaatgctaaaacca
taatagtacagctgaaccaatctgtagaaattaattgtacaagacccaacaacaatacaagaaaaagtatc
cgtatccagagaggaccagggagagcatttgttacaataggaaaaataggaaatatgagacaagcacattg
taacattagtagagcaaaatggaataacactttaaaacagatagatagcaaattaagagaacaatttggaa
ataataaaacaataatctttaagcagtcctcaggaggggacccagaaattgtaacgcacagttttaattgt
ggaggggaatttttctactgtaattcaacacaactgtttaatagtacttggtttaatagtacttggagtac
taaagggtcaaataacactgaaggaagtgacacaatcaccctcccatgcagaataaaacaaattataaaca
tgtggcaggaagtaggaaaagcaatgtatgcccctcccatcagtggacaaattagatgttcatcaaatatt
acagggctgctattaacaagagatggtggtaatagcaacaatgagtccgagatcttcagacctggaggagg
agatatgagggacaattggagaagtgaattatataaatataaagtagtaaaaattgaaccattaggagtag
cacccaccaaggcaaagagaagagtggtgcagACTAGTgcagtgggaataggagctttgttccttgggttc
t
ΔCleavage site (agagaaaaaaga)→SpeI
tgggagcagcaggaagcactatgggcgcagcgtcaatgacgctgacggtacaggccagacaattattgtct
ggtatagtgcagcagcagaacaatttgctgagggctattgaggcgcaacagcatctgttgcaactcacagt
ctggggcatcaagcagctccaggcaagaatcctggctgtggaaagatacctaaaggatcaacagctcctgg
ggatttggggttgctctggaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaataaa
tctctggaacagatttggaataacatgacctggatggagtgggacagagaaattaacaattacacaagctt
aatacactccttaattgaagaatcgcaaaaccagcaagaaaagaatgaacaagaattattggaattagata
aatgggcaagtttgtggaattggtttaacataacaaattggctgtggtatataaaattattcataatgata
gtaggaggcttggtaggtttaagaatagtttttgctgtactttctgtagtgaatagagttaggcagggata
ttcaccattatcgtttcagacccacctcccaatcccgaggggacccgacaggcccgaaggaatagaagaag
aaggtggagagagagacagagacagatccattcgattagtgaacggatccttagcacttatctgggacgat
ctgcggagcctgtgcctcttcagctaccaccgcttgagagacttactcttgattgtaacgaggattgtgga
acttctgggacgcagggggtgggaagccctcaaatattggtggaatctcctacagtattggagtcaggagc
taaagaatagtgctgttagcttgctcaatgccacagctatagcagtagctgaggggacagatagggttata
gaagtagtacaaggagcttatagagctattcgccacatacctagaagaataagacagggcttggaaaggat
tttgctataagatgggtggcaagtggtcaaaaagtagtgtggttggatggcctgctgtaagggaaagaatg
agacgagctgagccagcagcagatggggtgggagcagcatctcgagacctagaaaaacatggagcaatcac
aagtagcaacacagcagctaacaatgctgattgtgcctggctagaagcacaagaggaggaggaggtgggtt
ttccagtcacacctcaggtacctttaagaccaatgacttacaaggcagctgtagatcttagccacttttta
aaagaaaaggggggactggaagggctaattcactcccaacgaagacaagatatccttgatctgtggatcta
ccacacacaaggctacttccctgattag

FIGURE 45

DNA Sequence of $E^{m}\Delta C.N$ (Strain BH10) [SEQ ID NO: 22]:

```
Gaattcgccaccatgggagtgaaggagaaatatcagcacttgtggagatgg
EcoRI   Kozak  NcoI
gggtggagatggggcaccatgctccttgggatgttgatgatctgtagtgctacagaaaaattgtgggtcac
agtctattatggggtacctgtgtggaaggaagcaaccacctcttatttgtgcatcagatgctaaagcat
atgatacagaggtacataatgtttgggccacacatgcctgtgtacccacagaccccaccccacaagaagta
gtattggtaaatgtgacagaaaatttttaacatgtggaaaaatgacatggtagaacagatgcatgaggatat
aatcagtttatgggatcaaagcctaaagccatgtgtaaaattaaccccactctgtgttagtttaaagtgca
ctgatttgaagaatgatactaatacccaatagtagtagcgggagaatgataatggagaaaggagagataaaa
aactgctctttcaatatcagcacaagcataagaggtaaggtgcagaaagaatatgcatttttttataaact
tgatataatacccaatagataatgatactaccagctatacgttgacaagttgtaacacctcagtcattacac
agggcctgtccaaaggtatcctttgagccaattcccatacatattattgtgccccgggctggttttgcgattcta
aaatgtaatataatagacgttcaatggaacaggaccatgtacaaaatgtcagcacagtacaatgtacacatgg
aattaggccagtagtatcaactcaactgctgttaaatggcagtctggcagaagaagaggtagtaattagat
ctgccaatttcacagacaatgctaaaacatataattgatacagctgaacccaatctgtagaaaattaattgtaca
agacccaacaacaatacaagaaaaagtatccgtatccagagaggaccagggagagcatttgttacaatagg
aaaaatagggaaatatgagacaagcacattgtaacattagtagagcaaaatggaataacacttaaaacaga
tagatagcaaatttaagagaacaatttggaaataataaaacaataatctttaagcagtcctcaggaggggac
ccagaaattgtaacgcacagttttaattgtggaggggaatttttctcatgtaatttcaacacaactgtttaa
tagtacttggtttaatagtacttggagtactaaagggtcaaataacactgaaggaagtgacacaatcaccc
tcccatgcagaataaaacaaattataaacatgtggcaggaagtaggaaaagcaatgtatgccccctcccatc
agtggacaaattagatgttcatcaaatattacagggctgctattaacaagagatggtggtaatagcaacaa
tgagtccgagatcttcagacctggaggaggagatatgagggacaattggagaagtgaattatataaatata
aagtagtaaaaattgaacccattaggagtagcacccaccaccaaggcaaagagagagatggtgtgcagACTAGTgca
gtcgggaatcaggagctttgttccttgggtcttgggagc
                ΔCleavage site(aggaaaaaagg)→SpeI
agcaggaagcactatgggcgcagcgtcaatgacgctgacggtacaggccagacaattattgtctggtatag
tgcagcagcagaacaatttgctgagggctattgaggcgcaacagcatctgttgcaactcacagtctggggc
atcaagcagctccaggcaagaatcctggctgtggaaagatacctaaaggatcaacagctcctggggatttg
gggttgctctggaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaataaatctctgg
aacagatttggaataacatgacctggatggagtgggacagagaaattaacaattacacaagcttaatacac
tccttaattgaagaatcgcaaaaccagcaagaaaagaatgaacaagaattattggaattagataaatgggc
aagtttgtggaattggtttaacataacaaattggctgtggtatataaaattattcataatgatagtaggag
gcttggtaggtttaagaatagtttttgctgtactttctgtagtgaatagagttaggcagggatattcacca
ttatcgtttcagacccacctcccaatcccgaggggacccgacaggcccgaaggaatagaagaagaaggtgg
agagagagacagacagatccattcgattagtgaacggatcctttagcactaatcgggacgatctgcgga
gcctgtgcctcttcagctaccaccgcttgagagactactcttgattgtaacgaggattgtggaacttctg
ggacgcagggggtgggaagccctcaaatattggtggaatctcctacagtattggagtcaggagctaaagaa
tagtgctgttagcttgctcaatgccacagctatagcagtagctgagggacagatagggttatagaagtag
tacaaggacgttatagagctattcgccacatacctagaagaataagacagggcttggaaaggatttttgcta
taagatgggtggcaagtggtcaaaaagtagtgtggttggatggcctgctgtaagggaaagaatgagacgag
ctgagccagcagcagatgggggtgggagcagcatctcgagacctagaaaaacatggagcaatcacaagtagc
aacacagcagctaacaatgctgattgtgcctggctagaagcacaagaggaggagggtgggttttccagt
cacacctcaggtacctttaagaccaatgacttacaaggcagctgtagatcttagccactttttaaaagaaa
aggggggactggaagggctaattcactcccaacgaagacaagatatccttgatctgtggatctaccacaca
caaggctacttccctgattag
```

FIGURE 46

DNA Sequence of $E^{m}\Delta C\Delta T^{300}$.T (BH10) [SEQ ID NO: 23]:

```
Gaattctgcaacaactgctgtttatccattttcagaattgggtgtcgacat
EcoRI
Agcagaataggcgttactcgacagaggagagcaagaaatggagccagtaga
                                        Tat 1
tcctagactagagccctggaagcatccaggaagtcagcctaaaactgcttgtaccaattgctattgtaaaa
agtgttgctttcattgccaagtttgtttcataacaaaagccttaggcatctcctatggcaggaagaagcgg
agacagcgacgaagacctcctcaaggcagtcagactcatcaagtttctctatcaaagcagtaagtagtaca
tgtaatgcaacctatacaaatagcaatagtagcattagtagtagcaataataatagcaatagttgtgtggt
ccatagtaatcatagaatatagaggaaaatattaagacaaagaaaaatagacaggttaattgatagactaata
gaaagagcagaagacagtggcaatgagagtgaaggagaaatatcagcacttgtggagatgtgggtggagat
ggggcaccatgctccttgggatgttgatgatctgtagtgctacagaaaaattgttgggtcacagtctattat
gggtacctgtgtggaaggaagcaaccaccactctatttgtgcatcagatgctaaagcatatgatacaga
ggtacataattgttgggccacacacagccctgtgtacccacagaccccaacccacaagaagtagtattggtaa
atgtgacagaaaatttaacacgcggaaaaatgcagctggtagaacagatgcatgaggatataatcagttta
tgggatcaaagcctaaagccatgtgtaaaattaacccctcactctgtgttagtttaaagtgcactgatttgaa
gaatgatactaatacccaatagtagtagcgggagaatgataatggagaaaggagagataaaaaactgctctt
tcaatatcagcacaagcataagaggtaaggtgcagaaagaatatgcatttttttataaacttgatataata
ccaatagataatgatactaccagctatacgttgacaagttgtaacacctcagtcattacacaggcctgtcc
aaaggtatcctttgagccaatttcccatacattattgtgcccccgctggttttgcgatttctaaaatgtaata
ataagacgttcaatggaacaggaccatgtacaaatgtcagcacagtacaatgtacacatggaatttaggcca
gtagtatccaactcaactgctgttaaatggcagtctggcagaagaagaggtagtaattagatctgccaattt
cacagacaatgctaaaacccatagtagtacagctgaaccaatctgtagaaattaatttgtacaagacccaaca
acaatacaagaaaaagtatccgtatccagagaggaccagggagagcatttgttacaatagggaaaaatagga
aatatgagacaagcacattgtaacattagtagagcaaaatggaataacacttaaaacagatagatagcaa
attaagagaacaattctggaaatataaaacaataatcctttaagcagtcctcaggaggggacccagaaattg
taacgcacagttttaattgtggaggggaatttttcctcactgtaattcaacacaactgttaatagtacttgg
tttaatagtacttggagtactaaaggtcaaatAacactgaaggaagtgacacaatcacccccccatgcag
aataaaacaaattataaacatgtggcaggaagtaggaaaagcaatgtatgcccctccatcagtggacaaa
ttagatgttcatcaaatattacagggctgctattaacaagagatggtggtaatagcaacaatgagtccgag
atcttcagacctggaggaggagatatgagggacaattggagaagtgaattatataaaatataaagtagtaaa
aattgaaccattaggagtagcacccaccaaggcaaagagaagagtggtgcagACTAGTgcagtggaatag
gagctttgttccttgggttc
      ΔCleavage site(agaggaaaaaaga)→SpeI
ttgggagcagcaggaagcactatgggcgcagcgtcaatgacgctgacggtacaggccagacaattattgtc
tggtatagtgcagcagcagaacaatttgctgagggctattgaggcgcaacagcatctgttgcaactcacag
tctggggcatcaagcagctccaggcaagaatcctggctgtggaaagatacctaaaggatcaacagctcctg
gggatttgggttgctctggaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaataa
atctctggaacagatttggaatAacatgacctggatggagtgggacagagaaattaacaattacacaagct
taatacactcctaattgaagaatcgcaaaaccagcaagaaaagaatgaacaagaattattggaattagat
aaatgggcaagtttgtggaattggtttaacataacaaattggctgtggtatataaaattattcataatgat
agtaggaggcttggtaggttaagaatagtttttgctgtactttctgtagtgaatagagttaggcagggat
attcaccattatcgtttcagacccacctcccaatcccgaggggacccgacaggcccgaaggaatagaagaa
gaaggtggagagagagcagagacagatccattcgattagtgaacggatccttagcacttatctggtaa
```

Figure 47

DNA Sequence of E^m/E^m (BH10) [SEQ ID NO: 24]:

Gaattcgccaccatggagtgaaggagaaatatcagcacttgtggagatgg
EcoRI Kozak NcoI

gggtggagatggggcaccatgctccttgggatgttgatgatctgtagtgctacagaaaaattgtgggtcac
agtctattatggggtacctgtgtggaaggaagcaaccaccactctatttttgtgcatcagatgctaaagcat
atgatacagaggtacataatgtttgggccacacatgcctgtgtacccacagaccccaacccacaagaagta
gtattggtaaatgtgacagaaaaatttaacatgtggaaaaatgacatggtagaacagatgcatgaggatat
aatcagtttatgggatcaaagcctaaagccatgtgtaaaattaacccccactctgtgttagtttaaagtgca
ctgatttgaagaatgatactaatacccaatagtagtagcgggagaatgataatggagaaaggagagatAaaa
aactgctctttcaatatcagcacagccataagagtaaggtgcagaaagaatatgcatttttttataaact
tgatataatacccaatagataatgatactaccagctatacgttgacaagttgtaacacctcagtcattacac
aggcctgtccaaaggtatcctttgagccaatttcccatacattattgtgcccccggctggtttgccgatcta
aaatgtaataataagacgttcaatggaacagaccatgtacaaatgtcagcacagtacaatgtacacatgg
aattaggccagtagtatcaactcaactgctgttaaatggcagtctggcagaagaagaggtagtaattagat
ctgccaatttcacagacaatgctaaaaccataatagtacagctgaaccaatctgtgaaaattaattgtaca
agacccaacaacaatacaagaaaaagtatccgtatccagagaggaccagggagagcatttgttacaatagg
aaaaatagggaaatatgagacaagcacattgtaacattagagagcaaaatggaaataacacttaaaacaga
tagatagcaaattaagagaacaatttggaaataataaaacaataatctttaagcagtcctcaggaggggac
ccagaaattgtaacgcacagttttaattgtggagggggaatttttctcactgtaatttcaacacaactgtttaa
tagtacttggtttaatagtacttggagtactaaagggtcaaataacactgaaggaagtgacacaatcaccc
tcccatgcagaataaaacaaattataaacatgtggcaggaagtaggaaaagcaatgtatgcccctcccatc
agtggacaaattagatgttcatcaaatattacagggctgctattaacaagagatggtggtaatagcaacaa
tgagtccgagatcttcagacctggaggaggagatatgagggacaattggagaagtgaatttataaatata
aagtagtaaaaattgaaccattaggagtagcacccaccaagggcaaagagaagagtggtgcagagagaaaaa
agagcagtgggaatagggagcttttgttccttgggttcttgggagcagcaggaagcactatgggcgcagcgtc
aatgacgctgacggtacaggccagacaattattgtctggtatagtgcagcagcagaacaatttgctgaggg
ctattgaggcgcaacagcatctgttgcaactcacagtctggggcatcaagcagctccaggcaagaatcctg
gctgtggaaagatacctaaaggatcaacagctcctggggatttggggttgctctgaggaaactcatttgcac
cactgctgtgccttggaatgctagttggagtaataaatctctggaacagatttggaatacatgacctgga
tggagtgggacagagaaattaacaattacacaagcttaatacactccttaattgaagaatcgcaaaaccag
caagaaaagaatgaacaagaattattggaattagataaatgggcaagtttgtggaattggttaacataac
aaattggctgtggtatataaaattattcataatgatagtaggaggcttggtaggtttaagaatagtttttg
ctgtactttctgtagtgaatagagttaggcagggatattcaccattatcgtttcagacccacctcccaatc
ccgaggggacccgacaggcccgaaggaatagaagaagaaggtggagagagagacagagacagatccattcg
attagtgaacggatcctagcactcatctgggacgacctggggagcctgtgcctcttcagctaccaccgct
tgagagacttactcttgattgtaacgaggattg-ggaacttctgggacgcagggggtgggaagccctcaaa
tattggtggaatctcctacagtattggagtcaggagctaaagaatagtgctgttagcttgctcaatgccac
agctatagcagtagctgaggggacagatagggttatagaagtagtacaaggagcttatagagctattcgcc
acatacctagaagaataagacagggcttggaaaggattttgctataa

FIGURE 48

Sequences of V3 loop Multi-clade HIV-1 Clones:

Clade	ACC#	HIV-1 Strain	From(nt)	To(nt)
B	M15654	BH10	885	992
A	U09127	192UG037WHO.01083hED	888	992
C	U09126	192BR025WHO.01093hED	876	980
D	U43386	192UG024.2	888	989
E	U08458	193TH976.17	894	998
F	U27401	193BR020.17	888	992
G	U30312	192RU131.9	885	989

Tgtacaagacccaacaacaatacaagaaaaagtatccgtatccagagagga
ccaggggagagcatttgttacaataggaaaaatagggaaatatgagacaagca
cattgt **Clade B [SEQ ID NO: 25]**

Tgtaccagacctaacaacaatacaagaaaaagtgtacgtataggaccagga
caaacattctatgcaacaggtgatataataggggatataagacaagcacat
tgt **Clade A [SEQ ID NO: 26]**

Tgtacgagacccaacaataatacaagaaaaagtataaggataggaccagga
caagcattctatgcaacaggagaaataataggagatataagacaagcacat
tgt **Clade C [SEQ ID NO: 27]**

Tgcacaaggccctacaacaatataagacaaaggacccccataggactaggg
caagcactctatacaacaagaagaatagaagatataagaagagcacattgt
Clade D [SEQ ID NO: 28]

Tgtaccagaccctccaccaatacaagaacaagtatacgtataggaccagga
caagtattctatagaacaggagacataacaggagatataagaaaagcatat
tgt **Clade E [SEQ ID NO: 29]**

Tgtacaagacccaacaacaatacaagaaaaagaatatctttaggaccagga
cgagtattttatacagcaggagaaataataggagacatcagaaaggcacat
tgt **Clade F [SEQ ID NO: 30]**

Tgtaccagacctaataacaatacaagaaaaagtataacttttgcaccagga
caagcgctctatgcaacaggtgaaataataggagatataagacaagcacat
tgt **Clade G [SEQ ID NO: 31]**

FIGURE 49A

DNA sequence of modified Env including multi-clade V3 loops [SEQ ID NO: 32]:

```
Atgagagtgaaggagaaatatcagcacttgtggagatggggtggagatggggcaccatgctccttgggat
gttgatgatctgtagtgctacagaaaaattgtgggtcacagtctattatggggtacctgtgtggaaggaag
caaccaccactctattttgtgcatcagatgctaaagcatatgatacagaggtacataatgtttgggccaca
catgcctgtgtacccacagaccccaacccacaagaagtagtattggtaaatgtgacagaaaatttaacat
gtggaaaaatgacatggtagaacacgatgcatgaggatataatcagtttatgggatcaaagcctaaagccat
gtgtaaaattaaccccactctgtgttggagctggtagttgtaacaccctcagt
                    V1, V2 deletion, GAG insertion
Cattacacaggcctgtccaaaggtatcctttgagccaattcccatacattattgtgccccggctggttttg
cgattctaaaatgtaataataagacgttcaatggaacaggaccatgtacaaatgtcagcacagtacaatgt
acacatggaattaggccagtagtatcaactcaactgctgttaaatggcagtctagcagaagaagaggtagt
aattagatctgccaattttcacagacaatgctaaaacctataatagtacagctgaaccaatctgtagaaatta
attgtacaagacccaacaacaa
Start of Clade B
Tacaagaaaaagtatccgtatccagagaggaccagggagagcatttgttacaatagggaaaaataggaaata
tgagacaagcacattgtctcgggtgtaccag
          Insert a AvaI site       Clade A
Acctaacaacaatacaagaaaaagtgtacgtatagggaccaggacaaacattctatgcaacaggtgatataa
taggggatataagacaagcacattgttgtac
                    Clade C
Gagacccaacaataatacaagaaaaagtataaggataggaccaggacaagcattctatgcaacaggagaaa
taataggagatataagacaagcacattgttg
                    Clade D
Cacaaggccctacaacaatataagacaaaggacccccatagggactagggcaagcactctatacaacaagaa
gaatagaagatataagaagagcacattgttg
                    Clade E
Taccagaccctccaccaatacaagaacaagtatacgtatagggaccaggacaagtattctatagaacaggag
acatacaggagatataagaaaagcatattgtggatcctgtacaagacccaacaacaatacaagaaaaaga
atatctttagg
                         BamHI   clade F
Accaggacgagtattttatacagcaggagaaataataggagacatcagaaaggcacattgttgtaccagac
ctaataacaatacaagaaaaagtataacttt
                                                    Clade G
Tgcaccaggacaagcgctctatgcaacaggtgaaataatagggagatataagacaagcacattgtctcggga
acattagtagagcaaaatggaataacactt
                                                    Insert a AvaI
Aaaacagatagatagcaaattaagagaacaatttggaaataataaaacaataatccttaagcagtcctcag
gaggggacccagaaattgtaacgcacagttttaattgtggaggggaatttttctactgtaattcaacacaa
ctgtttaatagtacttggtttaatagtacttggagtactaaaggtcaaataacactgaaggaagtgacac
aatcaccctcccatgcagaataaaacaaattataaacatgtggcaggaagtaggaaaagcaatgtatgccc
ctcccatcagtggacaaattagatgttcatcaaatattacagggctgctattaacaagagatggtggtaat
agcaacaatgagtccgagatcttcagacctggaggaggagatatgagggacaattggagaagtgaattata
taaatataaagtagtaaaaattgaaccattaggagtagcacccaccaaggcaaagagaagagtggtgcaga
gagctagtgcagtggg
Cleavage site mutation (SpeI)
Aataggagctttgttccttgggttcttgggagcagcaggaagcactatgggcgcagcgtcaatgacgctga
cggtacaggccagacaattattgtctggtatagtgcagcagcagaacaatttgctgagggctattgaggcg
caacagcatctgttgcaactcacagtctggggcatcaagcagctccaggcaagaatcctggctgtggaaag
atacctaaaggatcaacagctcctggggatttggggttgctctggaaaactcatttgcaccactgctgtgc
cttggaatgctagttggagtaataaatctctggaacagatttggaatcacatgacctggatggagtgggac
agagaaattaacaattacacaagcttaatacactccttaattgaagaatcgcaaaaccagcaagaaaagaa
tgaacaagaattattggaattagataaatgggcaagtttgtggaattggtttaacataacaaattggctgt
ggtatataaaatcgtggctgctgctgctcctgctttcccttctcccttcctcccaggccacggatttcatgtcc
gtgtgaa                GPI anchor
```

FIGURE 49B

Amino acid sequence of modified Env including multi-clade V3 loops [SEQ ID NO: 33]:

M R V K E K Y Q H L W R W G W R W G
T M L L G M L M I C S A T E K L W V
T V Y Y G V P V W K E A T T T L F C
A S D A K A Y D T E V H N V W A T H
A C V P T D P N P Q E V V L V N V T
E N F N M W K N D M V E Q M H E D I
I S L W D Q S L K P C V K L T P L C
V G A G S C N T S V I T Q A C P K V
S F E P I P I H Y C A P A G F A I L
K C N N K T F N G T G P C T N V S T
V Q C T H G I R P V V S T Q L L L N
G S L A E E E V V I R S A N F T D N
A K T I I V Q L N Q S V E I N C T R
P N N N T R K S I R I Q R G P G R A
F V T I G K I G N M R Q A H C L G C
T R P N N N T R K S V R I G P G Q T
F Y A T G D I I G D I R Q A H C C T
R P N N N T R K S I R I G P G Q A F
Y A T G E I I G D I R Q A H C C T R
P Y N N I R Q R T P I G L G Q A L Y
T T R R I E D I R R A H C C T R P S
T N T R T S I R I G P G Q V F Y R T
G D I T G D I R K A Y C G S C T R P
N N N T R K R I S L G P G R V F Y T
A G E I I G D I R K A H C C T R P N
N N T R K S I T F A P G Q A L Y A T
G E I I G D I R Q A H C L G N I S R
A K W N N T L K Q I D S K L R E Q F
G N N K T I I F K Q S S G G D P E I
V T H S F N C G G E F F Y C N S T Q
L F N S T W F N S T W S T K G S N N
T E G S D T I T L P C R I K Q I I N
M W Q E V G K A M Y A P P I S G Q I
R C S S N I T G L L L T R D G G N S
N N E S E I F R P G G G D M R D N W
R S E L Y K Y K V V K I E P L G V A
P T K A K R R V V Q T S A V G I G A
L F L G F L G A A G S T M G A A S M
T L T V Q A R Q L L S G I V Q Q Q N
N L L R A I E A Q Q H L L Q L T V W
G I K Q L Q A R I L A V E R Y L K D
Q Q L L G I W G C S G K L I C T T A
V P W N A S W S N K S L E Q I W N N
M T W M E W D R E I N N Y T S L I H
S L I E E S Q N Q Q E K N E Q E L L
E L D K W A S L W N W F N I T N W L
W Y I K S W L L L L L L S L S L L Q
A T D F M S L *

FIGURE 50A

1. DNA sequence of p17/24 in natural form [SEQ ID NO: 34]:

atggtgcgagagcgtcagtattaagcgggggagaattagatcgatgggaaaaaattcggttaaggccagg
gggaaagaaaaaatataaattaaaacatatagtatgggcaagcagggagctagaacgattcgcagttaatc
ctggcctgttagaaacatcagaaggctgtagacaaatactgggacagctacaaccatcccttcagacagga
tcagaaagaacttagatcattatataatacagtagcaaccctctattgtgtgcatcaaaggatagagataaa
agacaccaaggaagctttagacaagatagaggaagagcaaacaaaagtaagaaaaaagcacagcaagcag
cagctgacacaggacacagcagtcaggtcagccaaaattacccctatagtgcagaacatccagggggcaaatg
gtcacatcaggccatatcacctagaactttaaatgcatgggtaaaagtagtagaagaggaaggctttcagccc
agaagtaatacccatgtttttcagcattatcagaaggagccaccccacaagatttaaacaccatgctaaaca
cagtgggggggacatcaagcagccatgcaaatgttaaaagagaccatcaatgaggaagctgcagaatgggat
agagtacatccagtgcatgcagggcctattgcaccagggccagatgagagaccaaggggaagtgacatagc
aggaactactagtacccttcaggaacaaataggatggatgacaaatcatccacctatcccagtaggagaaa
tttatgaaagatggataatcctgggattaaataaaatagtaagaatgtatagccctaccagcatttctggac
ataagacaaggaccaaaagaacctttagagactatgtagaccggttctatgaaaactctaagagccgagca
agcttcacaggaggtaaaaaattggatgacagaaaccttgttggtccaaaatgcgaacccagattgtaaga
ctatttaaaagcattgggaccagcggctacactagaagaaatgatgacagcatgtcagggagtaggagga
cccggccataaggcaagagtttgtgtaa

2. DNA sequence of p17/24 in secreted form [SEQ ID NO: 35]:

atgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatgg
gp120 signal peptide
ggcaccatgctccttgggatgttgatgatctgtagtgctggtgcgagagcg
p17/p24
tcagtattaagcgggggagaattagatcgatgggaaaaaattcggttaaggccagggggaaagaaaaaata
taaattaaaacatatagtatgggcaagcagggagctagaacgattcgcagttaatcctggcctgttagaaa
catcagaaggctgtagacaaatactgggacagctacaaccatcccttcagacaggatcagaagaacttaga
tcattatataatacagtagcaaccctctattgtgtgcatcaaaggatagagataaaagacaccaaggaagc
tttagacaagatagaggaagagcaaaacaaaagtaagaaaaaagcacagcaagcagctgacacaggac
acagcagtcaggtcagccaaaattacccctatagtgcagaacatccagggggcaaatggtacatcaggccata
tcacctagaactttaaatgcatgggtaaaagtagtagaagagaaggctttcagcccagaagtaatacccat
gttttcagcattatcagaaggagccaccccacaagatttaaacaccatgctaaacacagtgggggggacatc
aagcagccatgcaaatgttaaaagagaccatcaatgaggaagctgcagaatgggatagagtacatccagtg
catgcagggcctattgcaccaggccagatgagagaaccaaggggaagtgacatagcaggaactactagtac
ccttcaggaacaaataggatggatgacaaatcatccacctatcccagtaggagaaatttatgaaaagatgga
taatccctgggattaaataaaatagtaagaatgtatagccctaccagcatttctggacataagacaaggacca
aaagaacctttagagactatgtagaccggttctatgaaaactctaagagccgagcaagcttcacaggaggt
aaaaaattggatgacagaaaccttgttggtccaaaatgcgaacccagattgtaagactattttaaaagcat
tgggaccagcggctacactagaagaaatgatgacagcatgtcagggagtaggaggacccggccataaggca
agagtttgtgtaa

FIGURE 50A -continued

1. DNA sequence of p17/24 in membrane form (SEQ ID NO: 36]:

atgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatgg
gp120 signal peptide
Ggcaccatgctccttgggatgttgatgatctgtagtgctggtgcgagagcg
p17/p24
tcagtattaagcgggggagaattagatcgatgggaaaaaattcggttaaggccagggggaaagaaaaaata
taaattaaaacatatagtatgggcaagcagggagctagaacgattcgcagttaatcctggcctgttagaaa
catcagaaggctgtagacaaatactgggacagctacaaccatcccttcagacaggatcagaagaacttaga
tcattatataatacagtagcaaccctctattgtgtgcatcaaaggatagagataaaagacaccaaggaagc
tttagacaagatagaggaagagcaaaacaaaagtaagaaaaaagcacagcaagcagcagctgacacaggac
acagcagtcaggtcagccaaaattaccctatagtgcagaacatccagggqcaaatggtacatcaggccata
tcaccctagaactttaaatgcatgggtaaaagtagtagaagagaaggctttcagcccagaagtaataccccat
gttttcagcattatcagaaggagccaccccacaagatttaaacaccatgctaaacacagtgggggacatc
aagcagccatgcaaatgttaaaagagaccatcaatgaggaagctgcagaatgggatagagtacatccagtg
catgcagggcctattgcaccaggccagatgagagaaccaaggggaagtgacatagcaggaactactagtac
ccttcaggaacaaatagqatggatgacaaataatccacctatcccagtaggagaaatttataaaagatgga
taatcctgggattaaataaaatagtaagaatgtatagcccctaccagcattctggacataagacaaggacca
aaagaacctttagagactatgtagaccggttctataaaactctaagagccgagcaagcttcacaggaggt
aaaaaattggatgacagaaaccttgttggtccaaaatgcgaacccagattgtaagactatttaaaagcat
tgggaccagcgggctacactagaagaaatgatgacagcatgtcagggagtaggaggacccggccataaggca
agagttttg
ttattcataatgatagtaggaggcttggtaggtttaagaatagtttttgctgtactttctgtagtgaatag
agttaggcagggatattcaccattatcgtttcagacccacctcccaatcccgaggggatma
gp41 transmembrane domain

FIGURE 50B

1. Amino acid sequence of p17/24 in natural form [SEQ ID NO: 37]:

M	G	A	R	A	S	V	L	S	G	G	E	L	D	R	W	E	K
I	R	L	R	P	G	R	K	K	K	Y	K	L	K	H	I	V	W
A	S	R	E	L	E	G	F	V	V	N	P	L	L	L	E	T	S
E	G	C	R	Q	I	L	A	N	K	Q	P	G	L	Q	T	G	S
E	E	L	R	S	L	Y	Q	Q	A	A	T	L	Y	C	V	H	Q
R	I	E	I	K	D	T	N	A	A	L	L	D	I	E	E	E	Q
N	K	S	K	K	K	A	K	E	A	A	A	K	T	G	S	S	S
Q	V	S	Q	N	Y	P	Q	N	Q	N	I	D	G	Q	M	V	H
Q	I	S	S	P	R	T	I	N	A	W	V	A	T	G	E	E	K
A	F	S	P	E	V	T	P	M	N	S	K	L	E	Q	G	A	T
P	Q	D	L	N	T	T	L	L	E	V	V	G	W	E	D	A	M
Q	M	L	K	E	E	P	I	N	E	A	A	A	H	G	P	V	H
P	V	H	A	G	G	T	I	A	P	Q	E	Q	Q	E	W	R	S
D	I	A	G	I	T	P	S	T	L	E	R	M	E	R	I	M	N
D	P	P	I	V	P	T	G	I	I	S	I	Q	Q	I	I	R	L
N	K	I	V	P	R	V	Y	S	P	T	W	R	Y	D	T	Q	G
P	K	E	A	S	F	M	V	Y	T	D	L	E	T	I	K	R	Q
E	Q	A	N	P	Q	R	E	K	D	W	Y	S	F	T	T	L	R
N	A	E	E	M	D	E	C	K	T	I	S	R	T	L	K	L	L
L	E	L	*	M	M	V	T	A	C	Q	G	M	A	E	P	A	A
R	V												G	L	G	H	K

2. Amino acid sequence of p17/24 in secreted form [SEQ ID NO: 38]:

M	R	V	K	E	K	Y	Q	H	L	W	R	W	G	W	R	W	G
T	M	L	L	G	L	L	M	I	C	S	A	G	A	R	A	S	V
L	S	G	G	E	E	D	L	M	E	K	I	R	L	R	P	G	G
K	K	K	Y	K	K	K	L	H	H	W	A	S	R	E	L	E	R
F	A	V	N	P	L	L	L	I	V	S	E	G	L	R	Q	I	L
G	Q	T	Q	P	S	L	Q	T	T	G	E	E	L	R	S	L	Y
N	K	E	A	T	D	L	K	L	G	S	Q	N	I	K	K	K	T
K	E	Q	A	L	A	K	D	V	H	E	Q	R	E	I	K	O	A
Q	Q	Q	A	A	A	A	D	H	E	G	T	K	V	S	S	K	P
Q	Q	Q	A	A	A	A	D	S	S	S	T	Q	V	S	Q	N	P
Q	I	Q	V	A	N	A	D	H	H	S	G	Q	V	I	Q	N	P
I	V	N	A	N	I	G	T	S	M	V	Q	Q	V	S	Q	Y	P
L	M	Q	A	W	V	Q	G	V	V	H	Q	A	A	I	S	Y	R
P	N	F	T	S	A	K	L	S	E	K	E	F	S	D	P	E	V
L	M	E	A	V	G	H	G	E	G	T	Q	P	D	L	L	N	T
N	E	F	T	A	A	W	E	Q	A	A	Q	Q	V	H	K	E	T
A	P	E	G	Q	M	D	R	D	R	V	P	M	I	A	A	G	P
T	L	Q	E	K	Q	P	R	I	T	G	W	N	K	P	I	T	V
E	I	Y	K	S	R	I	W	I	I	T	M	L	E	I	V	P	G
S	P	T	D	R	K	F	A	L	D	I	G	N	P	K	E	S	R
Y	V	D	L	K	V	A	G	L	K	T	Q	L	K	Q	A	M	D
T	I	Q	G	V	G	P	G	A	P	P	A	R	E	E	E	T	V
C	Q							H	K	A	T	A	V	L	*		A

FIGURE 50B-continued

1. Amino acid sequence of p17/24 in membrane bound form [SEQ ID NO: 39]:

M	R	V	K	E	K	Y	Q	H	L	W	R	W	G	W	R	W	G
T	M	L	L	G	M	L	M	I	C	S	A	G	A	R	A	S	V
L	S	G	G	E	L	D	R	W	E	K	I	R	L	R	P	G	G
L	S	G	G	E	L	D	R	W	E	K	I	R	L	R	P	G	G
K	K	K	Y	K	L	K	H	I	V	W	A	S	R	E	L	E	R
F	A	V	N	P	G	L	L	E	T	S	E	G	C	R	Q	I	L
G	Q	L	Q	P	S	L	Q	T	G	S	E	E	L	R	S	L	Y
N	T	V	A	T	L	Y	C	V	H	Q	R	I	E	I	K	D	T
K	E	A	L	D	K	I	E	E	E	Q	N	K	S	K	K	K	A
Q	Q	A	A	A	D	T	G	H	S	S	Q	V	S	Q	N	Y	P
I	V	Q	N	I	Q	G	Q	M	V	H	Q	A	I	S	P	R	T
L	N	A	W	V	K	V	V	E	E	K	A	F	S	P	E	V	I
P	M	F	S	A	L	S	E	G	A	T	P	Q	D	L	N	T	M
L	N	T	V	G	G	H	Q	A	A	M	Q	M	L	K	E	T	I
N	E	E	A	A	E	W	D	R	V	H	P	V	H	A	G	P	I
A	P	G	Q	M	R	E	P	R	G	S	D	I	A	G	T	T	S
T	L	Q	E	Q	I	G	W	M	T	N	N	P	P	I	P	V	G
E	I	Y	K	R	W	I	I	L	G	L	N	K	I	V	R	M	Y
S	P	T	S	I	L	D	I	R	Q	G	P	K	E	P	F	R	D
Y	V	D	R	F	Y	K	T	L	R	A	E	Q	A	S	Q	E	V
K	N	W	M	T	E	T	L	L	V	Q	N	A	N	P	D	C	K
T	I	L	K	A	L	G	P	A	A	T	L	E	E	M	M	T	A
C	Q	G	V	G	G	P	G	H	K	A	R	V	L	L	F	I	M
I	V	G	G	L	V	G	L	R	I	V	F	A	V	L	S	V	V
N	R	V	R	Q	G	Y	S	P	L	S	F	Q	T	H	L	P	I
P	R	G	*														

FIGURE 51A

1. DNA sequence of p17 in natural form [SEQ ID NO: 40]:

```
atgggtgcgagagcgtcagtattaagcgggggagaattagatcgatcgggaaaaaattcg
gttaaggccaggggaaagaaaaaatataaatttaaaacatatagtatgggcaagcaggg
agctagaacgattcgcagttaatccctggcctgttagaaacatcagaaggctgtagacaa
atactgggacagctacaacccatcccttcagacaggatcagaagaacttagatcattata
taatacagtagcaaccctctattgtgtgcatcaaaggatagagataaaagacaccaagg
aagctttagacaagatagaggaagagcaaaacaaaagtaagaaaaaagcacagcaagca
gcagctgacacaggacacagcagtcaggtcagccaaaattactaa
```

2. DNA sequence of p17 in secreted form [SEQ ID NO: 41]:

```
atgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatgg
gp120 signal peptide
ggcaccatgctccttgggatgttgatgatctgtagtgctggtgcgagagcg
                                                  p17
tcagtattaagcgggggagaattagatcgatgggaaaaaattcggttaaggccaggggg
aaagaaaaaatataaattaaaacatatagtatgggcaagcagggagctagaacgattcg
cagttaatcctggcctgttagaaacatcagaaggctgtagacaaatactgggacagcta
caaccatcccttcagacaggatcagaagaacttagatcattatataatacagtagcaac
cctctattgtgtgcatcaaaggatagagataaaagacaccaaggaagctttagacaaga
tagaggaagagcaaaacaaaagtaagaaaaaagcacagcaagcagcagctgacacagga
cacagcagtcaggtcagccaaaattactaa
```

3. DNA sequence of p17 in membrane bound form [SEQ ID NO: 42]:

```
atgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatgg
gp120 signal peptide
ggcaccatgctccttgggatgttgatgatctgtagtgctggtgcgagagcg
                                                  p17
tcagtattaagcgggggagaattagatcgatgggaaaaaattcggttaaggccaggggg
aaagaaaaaatataaattaaaacatatagtatgggcaagcagggagctagaacgattcg
cagttaatcctggcctgttagaaacatcagaaggctgtagacaaatactgggacagcta
caaccatcccttcagacaggatcagaagaacttagatcattatataatacagtagcaac
cctctattgtgtgcatcaaaggatagagataaaagacaccaaggaagctttagacaaga
tagaggaagagcaaaacaaaagtaagaaaaaagcacagcaagcagcagctgacacagga
cacagcagtcaggtcagccaaaattac
ttattcataatgatagtaggaggcttggtaggtttaagaatagtttttgctgtactttc
tgtagtgaatagagttaggcagggatattcaccattatcgtttcagacccacctcccaa
tcccgaggggataa
gp41 transmembrane domain
```

FIGURE 51B

1. Amino acid sequence of p17 in natural form (SEQ ID NO: 43):

M G A R A S V L S G G E L I R W E K
I R L R P G G K K K H I K I V W W S
A S R E L E R F A V N P P G S L Q S
E G C R Q I L G Q L Q P T G H E Q
E E L R S L Y N T V A L D K V Q Q
R I E I K D T K E A L D K E E S Q
N K S K K K A Q Q A A A D T G H S
Q V S Q N Y *

2. Amino acid sequence of p17 in secreted form (SEQ ID NO: 44):

M R V K E K Y Q H L W R W G W R W G
T M L L G M L M I C S A G A R A S G V
L S G G E L D R W E K I A S G R E G G
K K K Y N P L H I T A E G C L R Q E R L
F A V N P G L L E T G S S E E E R R S I L Y
G Q L Q P S L Q T G S S E E E I E L K Y T
G Q L Q P S L Q T G S S E E R I K D A
N T V A L Y C V H Q N K S K K K Y *
K E E D K I E E E Q Q N K S K Q N
Q Q A A A D T G H S S Q V S Q

3. Amino acid sequence of p17 in membrane bound form (SEQ ID NO: 45):

M R V K E K Y Q H L W R W G W R W G
T M L L G M L M I C S A G A R A S G V
L S K G E K L D R W E K I A S G R E G G
K K K Y Q P T L V H Q K S E I R E L D
G Q T V A T L Y C V H Q N K S K K K Y T
N T V A L D K I E E S S Q V S Q N A L
K E Q A A D T G H Q Q N Q V I K S K D K Y V L
Q Q I M I V G R Q G Y S L R S V F Q T H
F I V N R V G L V G S L P L S F
S V L P I G *

FIGURE 52A

1. DNA sequence of p24 in natural form [SEQ ID NO: 46]:

atgcctatagtgcagaacatccaggggcaaatggtacatccaggccatatcaccttagaacttaaatgcatgg
gtaaaagtagtagaagagaaggctttcagcccagaagtaatacccatgttttcagcattatcagaaggagcc
acccacaagatttaaacaccatgctaaacacagtgggggacatcaagcagccatgcaaatgttaaaagag
accatcaatgaggaagctgcagaatgggatagagtcatcccagtgcatgcagggcctattgcaccaggccag
atgagagaaccaaggggaagtgacatagcaggaactactagtacccttcaggaacaaatagggatggatgaca
aataatcccacctatcccagtaggagaaatttataaaagatggataatc
ctgggattaaataaaacatggaagaatgtatagccctaccagcattctggacataagacaaggaccaaaagaa
ccttttagagactatgtagaccggttctataaaactctaagagccgagcaagcttcacaggaggtaaaaaat
tggatgacagaaaccttgttggtccaaaatgcgaacccagattgtaagactattttaaaagcattgggacca
gcggctacactagaagaaatgatgacagcatgtcagggagtaggaggacccggccataaggcaagagttttg
taa

2. DNA sequence of p24 in secreted form [SEQ ID NO: 47]:

atgagagtgaaggagaaatatcagcacttgtgagagatggggtggagatgg
gp120 signal peptide ggcaccatgcctttgggatgttgatgatctgtagtgcctcctatagtgcag
p24
aacatccaggggcaaatggtacatcaggccatatcaccttagaacttaaatgcatgggtaaaagtagtagaa
gagaaggctttcagcccagaagtaatacccatgttttcagcattatcagaaggaggccacccacaagattta
aacaccatgctaaacacagtgggggacatcaagcagccatgcaaatgttaaaagagaccatcaatgaggaa
gctgcagaatgggatagagtcatcccagtgcatgcagggcctattgcaccaggccagatgagagaaccaagg
ggaagtgacatagcaggaactactagtacccttcaggaacaaatagggatggatgacaaataatcccacctatc
ccagtaggagaaatttataaaagatggataatcctgggattaaataaaacatggaagaatgtatagccctacc
agcattctggacataagacaaggaccaaaagaaccttttagagactatgtagaccggttctataaaaactcta
agagccgagcaagcttcacaggaggtaaaaaattggatgacagaaaccttgttggtccaaaatgcgaaccca
gattgtaagactattttaaaagcattgggaccagcggctacactagaagaaatgatgacagcatgtcaggga
gtaggaggacccggccataaggcaagagttttgtaa

3. DNA sequence of p24 in membrane bound form [SEQ ID NO: 48]:

atgagagtgaaggagaaatatcagcacttgtgagagatggggtggagatgg
gp120 signal peptide ggcaccatgcctttgggatgttgatgatctgtagtgcctcctatagtgcag
p24
aacatccaggggcaaatggtacatcaggccatatcaccttagaacttaaatgcatgggtaaaagtagtagaa
gagaaggctttcagcccagaagtaatacccatgttttcagcattatcagaaggaggccacccacaagattta
aacaccatgctaaacacagtgggggacatcaagcagccatgcaaatgttaaaagagaccatcaatgaggaa
gctgcagaatgggatagagtcatcccagtgcatgcagggcctattgcaccaggccagatgagagaaccaagg
ggaagtgacatagcaggaactactagtacccttcaggaacaaatagggatggatgacaaataatcccacctatc
ccagtaggagaaatttataaaagatggataatcctgggattaaataaaacatggaagaatgtatagccctacc
agcattctggacataagacaaggaccaaaagaaccttttagagactatgtagaccggttctataaaaactcta
agagccgagcaagcttcacaggaggtaaaaaattggatgacagaaaccttgttggtccaaaatgcgaaccca
gattgtaagactattttaaaagcattgggaccagcggctacactagaagaaatgatgacagcatgtcaggga
gtaggaggacccggccataaggcaagagttttg
ttattcatcaatgatagtaggaggcttggtaggtttaagaatagtttttgctgtactttctatagtgaatagta
gttaggcagggatattcaccattatcgtttcagacccacctcccaatcccgaggggataa
gp41 transmembrane domain

FIGURE 52B

1. Amino acid sequence of p24 in natural form (SEQ ID NO: 49):

M	P	I	V	Q	N	I	Q	G	Q	M	V	H	Q	A	I	S	P
R	T	L	N	A	W	V	K	V	V	E	E	K	A	F	S	P	E
V	I	P	M	F	S	A	L	S	E	G	A	T	P	Q	D	L	N
T	M	L	N	T	V	G	G	H	Q	A	A	M	Q	M	L	K	E
T	I	N	E	E	A	A	E	W	D	R	V	H	P	V	H	A	G
P	I	A	P	G	Q	M	R	E	P	R	G	S	D	I	A	G	T
T	S	T	L	Q	E	Q	I	G	W	M	T	N	N	P	P	I	P
V	G	E	I	Y	K	R	W	I	I	L	G	L	N	K	I	V	R
M	Y	S	P	T	S	I	L	D	I	R	Q	G	P	K	E	P	F
R	D	Y	V	D	R	F	Y	K	T	L	R	A	E	Q	A	S	Q
E	V	K	N	W	M	T	E	T	L	L	V	Q	N	A	N	P	D
C	K	T	I	L	K	A	L	G	P	A	A	T	L	E	E	M	M
T	A	C	Q	G	V	G	G	P	G	H	K	A	R	V	L	*	

2. Amino acid sequence of p24 in secreted form (SEQ ID NO: 50):

M	R	V	K	E	K	Y	Q	H	L	W	R	W	G	W	R	W	G
T	M	L	L	G	M	L	M	I	C	S	A	P	I	V	Q	N	I
Q	G	Q	M	V	H	Q	A	I	S	P	R	T	L	N	A	W	V
K	V	V	E	E	K	A	F	S	P	E	V	I	P	M	F	S	A
L	S	E	G	A	T	P	Q	D	L	N	T	M	L	N	T	V	G
G	H	Q	A	A	M	Q	M	L	K	E	T	I	N	E	E	A	A
E	W	D	R	V	H	P	V	H	A	G	P	I	A	P	G	Q	M
R	E	P	R	G	S	D	I	A	G	T	T	S	T	L	Q	E	Q
I	G	W	M	T	N	N	P	P	I	P	V	G	E	I	Y	K	R
W	I	I	L	G	L	N	K	I	V	R	M	Y	S	P	T	S	I
L	D	I	R	Q	G	P	K	E	P	F	R	D	Y	V	D	R	F
Y	K	T	L	R	A	E	Q	A	S	Q	E	V	K	N	W	M	T
E	T	L	L	V	Q	N	A	N	P	D	C	K	T	I	L	K	A
L	G	P	A	A	T	L	E	E	M	M	T	A	C	Q	G	V	G
G	P	G	H	K	A	R	V	L	*								

3. Amino acid sequence of p24 in secreted form (SEQ ID NO: 51):

M	R	V	K	E	K	Y	Q	H	L	W	R	W	G	W	R	W	G
T	M	L	L	G	M	L	M	I	C	S	A	P	I	V	Q	N	I
Q	G	Q	M	V	H	Q	A	I	S	P	R	T	L	N	A	W	V
K	V	V	E	E	K	A	F	S	P	E	V	I	P	M	F	S	A
L	S	E	G	A	T	P	Q	D	L	N	T	M	L	N	T	V	G
G	H	Q	A	A	M	Q	M	L	K	E	T	I	N	E	E	A	A
R	E	P	R	G	S	D	I	A	G	T	T	S	T	L	Q	E	Q
I	G	W	M	T	N	N	P	P	I	P	V	G	E	I	Y	K	R
W	I	I	L	G	L	N	K	I	V	R	M	Y	S	P	T	S	I
L	D	I	R	Q	G	P	K	E	P	F	R	D	Y	V	D	R	F
Y	K	T	L	R	A	E	Q	A	S	Q	E	V	K	N	W	M	T
E	T	L	L	V	Q	N	A	N	P	D	C	K	T	I	L	K	A
L	G	P	A	A	T	L	E	E	M	M	T	A	C	Q	G	V	G
G	P	G	H	K	A	R	V	L	L	F	I	M	I	V	G	G	L
V	G	L	R	I	V	F	A	V	L	S	V	V	N	R	V	R	Q
G	Y	S	P	L	S	F	Q	T	H	L	P	I	P	R	G	*	

FIGURE 53A

DNA sequence of modified Env including multi-clade V3 loops and Tat (SEQ ID NO: 52):

Gaatttgtgcaacaactgctgtttatccatttt cagaattgggtgtcgacatagcagaataggcgt
tactcgacagaggagagcaagaaatggagccagtagatcctagactagagccc

Tat1

Tggaagcatccaggaagtcagcctaaaactgcttgtaccaattgctattgtaaaaagtgttgctt
tcatttgccaagtttgtttcataacaaaagccttaggcatctcctatggcaggaagaagcggagac
agcgacgaagacctcctcaaggcagtcagactcatcaagtttctctatcaaagcagtaagtagta
catgtaatgcaacctatacaaatagcaatagtagcattagtagtagcaataatagcaatagt
tgtgtggtccatagtaatcatagaatatagga aaatattaagacaaagaaaaatagacaggttaa
ttgatagactaatagaaagagcagaagacagtggcaatgagagtgaaggagaaatatcagcacctt
gtggagatgggggtggagatggg

Envelope

Gcaccatgctccttgggatgttgatgatctgtagtgctacagaaaaattgtgggtcacagtctat
tatggggtacctgtgtggaaggaagcaaccaccactctatttttgtgcatcagatgctaaagcata
tgatacagaggtacataatgtttgggccacacatgcctgtgtacccacagaccccaacccacaag
aagtagtattggtaaatgtgacagaaaattttaacatgtggaaaaatgacatggtagaacagatg
catgaggatataatcagtttatgggatcaaagcctaaagccatgtgtaaaattaaccccactctg
tgttggagctggtagttgtaacacctca
Delete V1V2, insert Gly,Ala,Gly
gtcattacacaggcctgtccaaaggtatcctttgagccaattcccatacattattgtgccccggc
tggttttgcgatttctaaaatgtaatataagacgttcaatggaacaggaccatgtacaaatgtca
gcacagtacaatgtacacatggaattaggccagtagtatcaactcaactgctgttaaatggcagt
ctggcagaagaagaggtagtaattagatctgccaatttcacagacaatgctaaaacatataagt
acagctgaaccaatctgtagaaattaattgtacaag

First multi-clade repeat

Acccaacaacaatacaagaaaaagtatccgtatccagagaggaccagggagagcatttgttacaa
taggaaaaatagga aatatgagacaagcacattgtctcgggtgtaccagacctaacaacaataca
agaaaaagtgtacgtatagga ccaggacaaacattctatgcaacaggtgatataatagggga tat
aagacaagcacattgttgtacgagacccaacaataatacaagaaaaagtataaggatagg accag
gagcaagcattctatgcaacaggagaaataatagga gatataagacaagcacattgttgcacaa
ggcccta caacaatataagacaaaggacccccataggactagggcaagcactctatacaacaaga
agaatagaagatataagaagagcacattgttgtaccagaccctcccaccaatacaagaacaagtat
acgtatagga ccaggacaagtattctatagaacaggagacatacagggagatataagaaaagcat
attgtggatcctgtacaagacccaacaacaatacaagaaaaagaatatctttaggaccaggacga
gtattttatacagcaggagaaataataggagacatcagaaaggcacattgttgtaccagacctaa
taacaatacaagaaaaagtataacttttgcaccaggacaagcgctctatgcaacaggtgaaataa

FIGURE 53A-continued

taggagatataagacaagcacattgtcttgggaacattagtagagcaaaatggaataacactt
AvaI site, end of two multi-clade repeat
Aaaacagatagatagcaaattaagagaacaatttggaaataataaacaataactttaagcagt
cctcaggaggggacccagaaattgtaacgcagagttttaattgtggaggggaatttttctactgt
aattcaacacaactgtttaatagtacttggtttaatagtacttggagtactaaaggtcaaataa
cactgaaggaagtgacacaatcacccctcccatgcagaataaaacaaattataaacatgtggcagg
aagtaggaaaagcaatgtatgcccctcccatcagtggacaaattagatgttcatcaaatattaca
gggctgctattaacaagagatggtggtaatagcaacaatgagtccgagatctttcagacctggagg
aggagatatgagggacaattggagaagtgaattatataaatataaagtagtaaaaattgaaccat
taggagtagcacccaccaaggcaaagagaagagtggtgcagactagtgcagtgggaatagggagct
ttgttccttgg
Delete the cleavage site, insert SpeI site
gttcttgggagcagcaggaagcactatgggcgcagcgtcaatgacgctgacggtacaggccagac
aattattgtctggtatagtgcagcagcagaacaatttgctgagggctattgaggcgcaacagcat
ctgttgcaacctcacagtctggggcatcaagcagctccaggcaagaatcctggctgtggaaagata
cctaaaggatcaacagctcctggggatttggggttgctctggaaaactcatttgcaccactgctg
tgccttggaatgctagttggagtaataaatctctggaacagatttggaatcacatgacctggatg
gagtgggacagagaaattaacaattacacaagcttaatacactccttaattgaagaatcgcaaaa
ccagcaagaaaagaatgaacaagaattattggaattagataaatgggcaagtttgtggaattggt
ttaacataacaaattggctgtggtatataaaattattcataatgatagtaggaggcttggtaggt
ttaagaatagtttttgctgtactttctgtagtgaatagagttaggcagggatattcaccattatc
gtttcagacccacctcccaatcccgaggggacccgacaggcccgaaggaatagaagaagaaggtg
gagagagagacagagacagatccattcgattagtgaacggatccttagcacttatctggtaa

gp41, delete the 300 bp at C-terminal

FIGURE 53B

Amino acid sequence of modified Env including multi-clade V3 loops and Tat [SEQ ID NO: 53]:

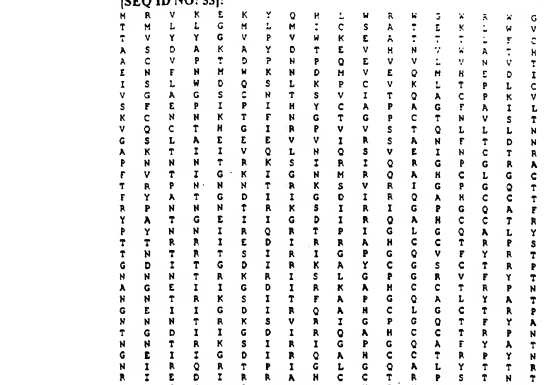


FIGURE 54A

DNA sequence of modified Env including multi-clade V3 loops, Tat and Rev [SEQ ID NO: 54]:

gaattctgcaacaactgctgtttatccatttttcagaattgggtgtcgacatagcagaat
aggcgttactcgacagaggagagcaagaaatggagccagtagatcctagactagagccc
Tat1
tggaagcatccaggaagtcagcctaaaactgcttgtaccaattgctattgtaaaaagtg
ttgctttcattgccaagtttgtttcataacaaaagccttaggcatctcctatggcagga
Rev1
agaagcggagacagcgacgaagacctcctcaaggcagtcagactcatcaagtttctcta
tcaaagcagtaagtagtacatgtaatgcaacctatacaaatagcaatagtagcattagt
agtagcaataataatagcaatagttgtgtggtccatagtaatcatagaatataggaaaa
tattaagacaaagaaaaatagacaggttaattgatagactaatagaaagagcagaagac
agtggcaatgagagtgaaggagaaatatcagcacttgtggagatgggggtggagatggg
Envelope
Gcaccatgctccttgggatgttgatgatctgtagtgctacagaaaaattgtgggtcaca
gtctattatggggtacctgtgtggaaggaagcaaccaccactctattttgtgcatcaga
tgctaaagcatatgatacagaggtacataatgttttgggccacacatgcctgtgtaccca
cagaccccaacccacaagaagtagtattggtaaatgtgacagaaaattttaacatgtgg
aaaaatgacatggtagaacagatgcatgaggatataatcagtttatgggatcaaagcct
aaagccatgtgtaaaattaaccccactctgtgttggagctggtagttgtaacacctca
Delete V1V2, insert Gly,ala,gly
gtcattacacaggcctgtccaaaggtatcctttgagccaattcccatacattattgtgc
cccggctggttttgcgattctaaaatgtaataataagacgttcaatggaacaggaccat
gtacaaatgtcagcacagtacaatgtacacatggaattaggccagtagtatcaactcaa
ctgctgttaaatggcagtctggcagaagaagaggtagtaattagatctgccaatttcac
agacaatgctaaaaccataatagtacagctgaaccaatctgtagaaattaattgtacaa
g
First multi-clades repeat
Acccaacaacaatacaagaaaaagtatccgtatccagagaggaccagggagagcatttg
ttacaatagggaaaaatagggaaatatgagacaagcacattgtctcgggtgtaccagacct
aacaacaatacaagaaaaagtgtacgtatagagaccaggacaaacattctatgcaacagg
tgatataatagggatataagacaagcacattgttgtacgagacccaacaataatacaa
gaaaaagtataaggataggaccaggacaagcattctatgcaacaggagaaataatagga
gatataagacaagcacattgttgcacaaggccctacaacaatataagacaaaggacccc
cataggactagggcaagcactctatacaacaagaagaatagaagatataagaagagcac
attgttgtaccagaccctccaccaatacaagaacaagtatacgtataggaccaggacaa
gtattctatagaacaggagacataacaggagatataagaaaagcatattgtggatcctg
tacaagacccaacaacaatacaagaaaaagaatatctttaggaccaggacgagtatttt
atacagcaggagaaataatagggagacatcagaaaggcacattgttgtaccagacctaat
aacaatacaagaaaaagtataacttttgcaccaggacaagcgctctatgcaacaggtga
aataatagggagatataagacaagcacattgttctcgggtgtaccagacctaacaacaata
Second multi-clade repeat
caagaaaaagtgtacgtatagggaccaggacaaacattctatgcaacaggtgatataata
ggggatataagacaagcacattgttgtacgagacccaacaatataacaagaaaaagtat

FIGURE 54A-continued

aaggataggaccaggacaagcattctatgcaacaggagaaataataggagatataagac
aagcacattgttgcacaaggccctacaacaatataagacaaaggacccccataggacta
gggcaagcactctatacaacaagaagaatagaagatataagaagagcacattgttgtac
cagaccctccaccaatacaagaacaagtatacgtatagaggaccaggacaagtattctata
gaacaggagacataacaggagatataagaaaagcatattgtggatcctgtacaagaccc
aacaacaatacaagaaaaagaatatctttaggaccaggacgagtattttatacagcagg
agaaataatagggagacatcagaaaggcacattgttgtaccagacctaataacaatacaa
gaaaaagtataacttttgcaccaggacaagcgctctatgcaacaggtgaaataatagga
gatataagacaagcacattgtctccgggaacattagtagagcaaaatggaataacacttt
AvaI site, end of two multi-clade repeat
Aaaacagatagatagcaaattaagagaacaatttggaaataataaaacaataatctttta
agcagtcctcaggaggggacccagaaatttgtaacgcacagttttaattgtggaggggaa
ttttttctactgtaattcaacacaactgtttaatagtacttggtttaatagtacttggag
tactaaagggtcaaataacactgaaggaagtgacacaatcacccctcccatgcagaataa
aacaaattataaacatgtggcaggaagtaggaaaagcaatgtatgcccctcccatcagt
ggacaaattagatgttcatcaaatattacagggctgctattaacaagagatggtggtaa
tagcaacaatgagtccgagatcttcagacctggaggaggagatatgagggacaattgga
gaagtgaattatataaatataaagtagtaaaaattgaaccattaggagtagcacccacc
aaggcaaagagaagagtggtgcagactagtgcagtgggaataggagctttgttccttgg
Delete the cleavage site, insert SpeI
gttcttgggagcagcaggaagcactatgggctgcacgtcaatgacgctgacggtacagg
ccagacaattattgtctgatatagtgcagcagcagaacaatttgctgagggctattgag
gcgcaacagcatctgttgcaactcacagtctggggcatcaaacagctccaggcaagaat
cctggctgtggaaagatacctaaaggatcaacagctcctggggatttggggttgctctg
gaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaataaatctctg
gaacagatttggaataacatgacctggatggagtgggacagagaaattaacaattacac
aagcttaatacactccttaattgaagaatcgcaaaaccagcaagaaaagaatgaacaag
aattattggaattagataaatgggcaagtttgtggaattggttaacataacaaattgg
ctgtggtatataaaattattcataatgatagtaggaggcttggtaggtttaagaatagt
ttttgctgtactttctatagtgaatagagttaggcagggatatttcaccattatcgtttc
agacccaccttcccaatcccgaggggacccgacaggcccgaaggaatagaagaagaaggt
ggagagagagacagagacagatccatttcgattagtgaacggatccttagcacttatctg
ggacgatctgcggagcctgtgcctcttcagctaccaccgcttgagagacttactcttga
ttgtaacgaggattgtggaacttctgggacgcagggggtgggaagccctcaaatattgg
tggaatctcctacagtattggagtcaggaactaaagaatagtgctgttaacttgctcaa
tgccacagccatagcagtagctgagtaa

gp41, but 99 bp truncation at C-terminal

FIGURE 54B

Amino acid sequence of modified Env including multi-clade V3 loops. Tat and Rev [SEQ ID NO: 55]:

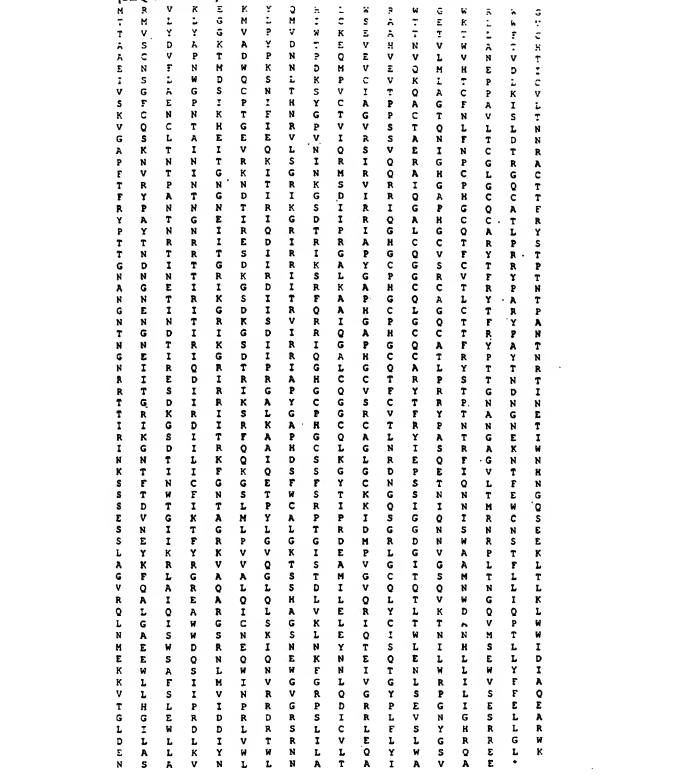


FIGURE 55A

DNA sequence of HIV-1 (strain BH10) Protease (PI, nt 1407-1907) [SEQ ID NO: 56]:

atgttctttagggaagatctggccttcctacaagggaaggccagggaattttcttcagagcagaccagagcca
acagccccaccatttcttcagagcagaccagagccaacagccccaccagaagagagcttcaggtctggggt
agagacaacaactccccctcagaagcaggagccgatagacaaggaactgtatcctttaacttccctcagatc
actcttttggcaacgaccccctcgtcacaataaagatagggggggcaactaaaggaagctctattagatacagga
gcagatgatacagtattagaagaaatgagtttgccaggaagatggaaaccaaaaatgatagggggaattgg
aggttttatcaaagtaagacagtatgatcagatactcatagaaatctgtggacataaagctataggtacagtatt
agtaggacctacacctgtcaacataattggaagaaatctgttgactcagattggttgcactttaaatttttaa

FIGURE 55B

Amino acid sequence of HIV-1 (strain BH10) Protease (PI) [SEQ ID NO: 57]:

M	F	F	R	E	D	L	A	F	L	Q	G	K	A	R	E	F	S
S	E	Q	T	R	A	N	S	P	T	I	S	F	E	Q	T	R	A
N	S	P	T	R	R	E	L	Q	V	W	G	R	D	N	N	S	P
S	E	A	G	A	D	R	Q	G	T	V	S	F	N	F	P	Q	I
T	L	W	Q	R	P	L	V	T	I	V	I	K	G	G	Q	K	E
A	L	L	D	T	G	A	D	T	D	V	L	V	E	N	H	L	P
G	R	W	K	P	K	M	I	G	G	I	G	G	H	G	I	V	R
Q	Y	D	Q	I	L	I	E	C	I	G	H	H	K	F	I	T	V
L	V	G	P	T	P	V	N	G	I	G	R	N	N	A	L	G	I
G	C	T	L	N	F	*								L		T	

FIGURE 56A

DNA sequence of HIV-1 (strain BH10) Gag-PI [SEQ ID NO: 58]:

Atgggtgcgagagcgtcagtattaagcgggggagaattagatcgatgggaaaaaattcg
gttaaggccaggggaaagaaaaatataaattaaaacatatagtatgggcaagcaggg
agctagaacgattcgcagttaatcctggcctgttagaaacatcagaaggctgtagacaa
atactgggacagctacaaccatccccttcagacaggatcagaagaacttagatcattata
taatacagtagcaaccctctattgtgtgcatcaaaggatagagataaaagacaccaagg
aagctttagacaagatagaggaagagcaaaacaaaagtaagaaaaaagcacagcaagca
gcagctgacacaggacacagcagtcaggtcagccaaaattacccctatagtgcagaacat
ccaggggcaaatggtacatcaggccatatcacctagaactttaaatgcatgggtaaaag
tagtagaagagaaggctttcagcccagaagtaatacccatgttttcagcattatcagaa
ggagccaccccacaagatttaaacaccatgctaaacacagtgggggacatcaagcagc
catgcaaatgttaaaagagaccatcaatgaggaagctgcagaatgggatagagtacatc
cagtgcatgcagggcctattgcaccaggccagatgagagaaccaaggggaagtgacata
gcaggaactactagtacccttcaggaacaaatagqatggatgacaaatAatccaccctat
cccagtaggagaaatttataaaagatggataatcctgggattaaataaaatagtaagaa
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taccataatgatgcagagaggcaattttaggaaccaaagaaagatggttaagtgtttca
attgtggcaaagaagggcacacagccagaaattgcagggccctaggaaaaagggctgt
tggaaaatgtggaaaggaaggacaccaaatgaaagattgtactgagagacaggctaattt
atttagggaagatctggccttcctacaagggaaggccagggaatttttcttcagagcaga
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caataaagataggggggcaactaaaggaagctctattagatacaggagcagatgatata
gtattagaagaaatgagtttgccaggaagatggaaaccaaaaatgatagggggaattgg
aggttttatcaaagtaagacagtatgatcagatactcatagaaatctgtggacataaag
ctataggtacagtattagtaggacctacacctgtcaacataattggaagaaatctgttg
actcagattggttgcactttaaatttttaa

FIGURE 56B

Amino acid sequence of HIV-1 (strain BH10) Gag-PI [SEQ ID NO: 59]:

M	G	A	R	A	S	V	L	S	G	G	E	L	D	R	W	E	K
I	R	L	R	P	G	G	K	K	K	Y	K	L	K	H	I	V	W
A	S	R	E	L	E	R	F	A	V	N	P	G	L	L	E	T	S
E	G	C	R	Q	I	L	G	Q	L	Q	P	S	L	Q	T	G	S
E	E	L	R	S	L	Y	N	T	V	A	T	L	Y	C	V	H	Q
R	I	E	I	K	D	T	K	E	A	L	D	K	I	E	E	E	Q
N	K	S	K	K	K	A	Q	Q	A	A	A	D	T	G	H	S	S
Q	V	S	Q	N	Y	P	I	V	Q	N	I	Q	G	Q	M	V	H
Q	A	I	S	P	R	T	L	N	A	W	V	K	V	V	E	E	K
A	F	S	P	E	V	I	P	M	F	S	A	L	S	E	G	A	T
P	Q	D	L	N	T	M	L	N	T	V	G	G	H	Q	A	A	M
Q	M	L	K	E	T	I	N	E	E	A	A	E	W	D	R	V	H
P	V	H	A	G	P	I	A	P	G	Q	M	R	E	P	R	G	S
D	I	A	G	T	T	S	T	L	Q	E	Q	I	G	W	M	T	N
N	P	P	I	P	V	G	E	I	Y	K	R	W	I	I	L	G	L
N	K	I	V	R	M	Y	S	P	T	S	I	L	D	I	R	Q	G
P	K	E	P	F	R	D	Y	V	D	R	F	Y	K	T	L	R	A
E	Q	A	S	Q	E	V	K	N	W	M	T	E	T	L	L	V	Q
N	A	N	P	D	C	K	T	I	L	K	A	L	G	P	A	A	T
L	E	E	M	M	T	A	C	Q	G	V	G	G	P	G	H	K	A
R	V	L	A	E	A	M	S	Q	V	T	N	T	A	T	I	M	M
Q	R	G	N	F	R	N	Q	R	K	M	V	K	C	F	N	C	G
K	E	G	H	T	A	R	N	C	R	A	P	R	K	K	G	C	W
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F	F	R	E	D	L	A	F	L	Q	G	K	A	R	E	F	S	S
E	Q	T	R	A	N	S	P	T	I	S	S	E	Q	T	R	A	N
S	P	T	R	R	E	L	Q	V	W	G	R	D	N	N	S	P	S
E	A	G	A	D	R	Q	G	T	V	S	F	N	F	P	Q	I	T
L	W	Q	R	P	L	V	T	I	K	I	G	G	Q	L	K	E	A
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Y	D	Q	I	L	I	E	I	C	G	H	K	A	I	G	T	V	L
V	G	P	T	P	V	N	I	I	G	R	N	L	L	T	Q	I	G
C	T	L	N	F	*												

FIGURE 57

Primers for multi-clade V3 loops:

Clade A: (1). forward primer A888F5 [SEQ ID NO: 60]:
5'-aaa tca acc gga att gaa ttc cct cgg gtg tac cag acc taa caa caa tac-3'
EcoRI AvaI
(2). reverse primer A-CR3 [SEQ ID NO: 61]:
5'-att gtt ggg tct cgt aca aca atg tgc ttg tct tat atc ccc-3'

Clade C: (3). forward primer A-CF5 [SEQ ID NO: 62]:
5'-ggg gat ata aga caa gca cat tgt acg aga ccc aac aat ac-3'
(4). reverse primer C980R3 [SEQ ID NO: 63]:
5'-gtt gta ggg cct tgt gca aca atg tgc ttg tct tat atc –3'

Clade D: (5). forward primer D888F5 [SEQ ID NO: 64]:
5'-gat ata aga caa gca cat tgt tgc aca agg ccc tac aac-3'
(6). reverse primer D-ER3 [SEQ ID NO: 65]:
5'-ggt gga ggg tct ggt aca aca atg tgc tct tct tat –3'

Clade E: (7). forward primer D-EF5 [SEQ ID NO: 66]:
5'-ata aga aga gca cat tgt tgt acc aga ccc tcc acc-3'
(8). reverse primer E998R3 [SEQ ID NO: 67]:
5'-gta ttg ttg ttg ggt ctt gta caa caa tat gct ttt ctt ata tct cc-3'

Clade F: (9). forward primer F888F5 [SEQ ID NO: 68]:
5'-gga gat ata aga aaa gca tat tgt tgt aca aga ccc aac aac aat ac-3'
(10). reverse primer F-GR3 [SEQ ID NO: 69]:
5'-gtt att agg tct ggt aca aca atg tgc ctt tct gat gtc-3'

Clade G: (11). forward primer F-GF5 [SEQ ID NO: 70]:
5'-gac atc aga aag gca cat tgt tgt acc aga cct aat aac-3'
(12). reverse primer G989R3 [SEQ ID NO: 71]:
5'-aat caa cta gtc tag acc ccc gag tct aga aca atg tgc ttg tct tat atc tcc-3'
AvaI XbaI

FIGURE 58

pRAd-ORF6-Gag/PI-RT

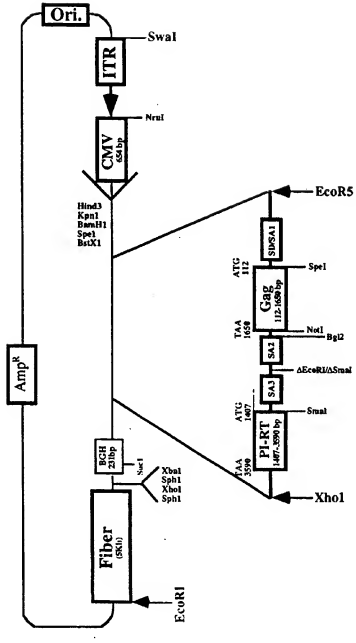


FIGURE 59

pRAd-ORF6-Gag-PI-RT

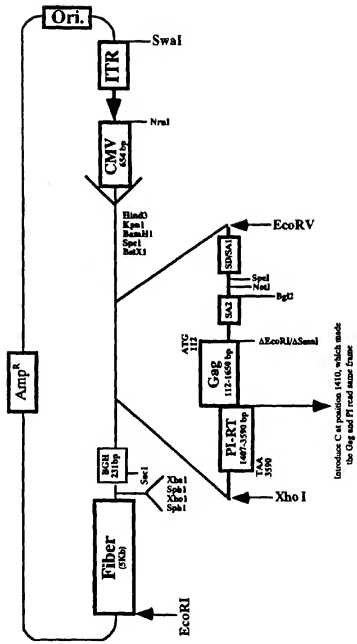


FIGURE 60

pRAd-ORF6-Gag/Pol

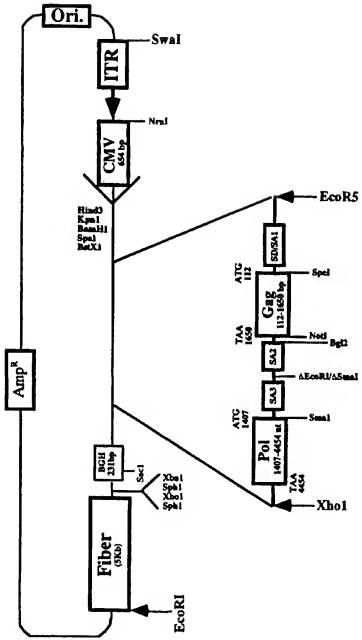
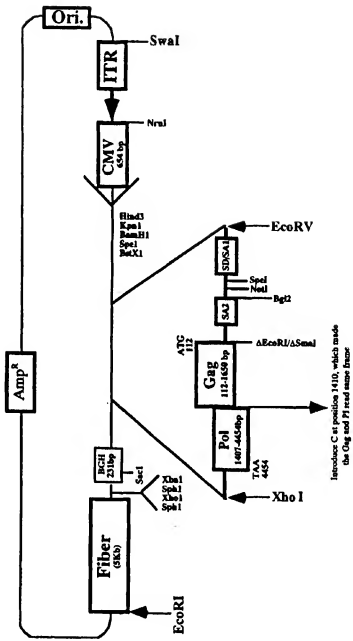


FIGURE 61

pRAd-ORF6-Gag-Pol



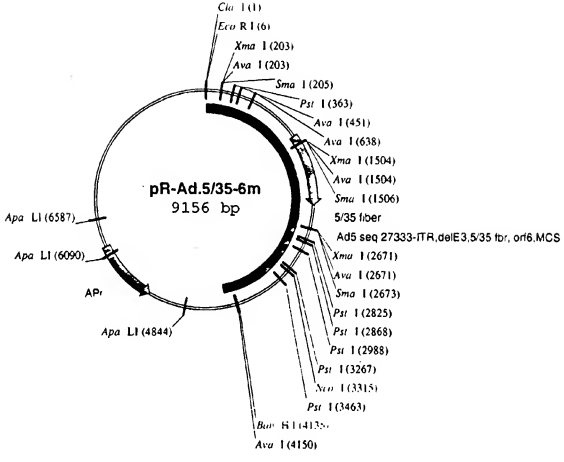

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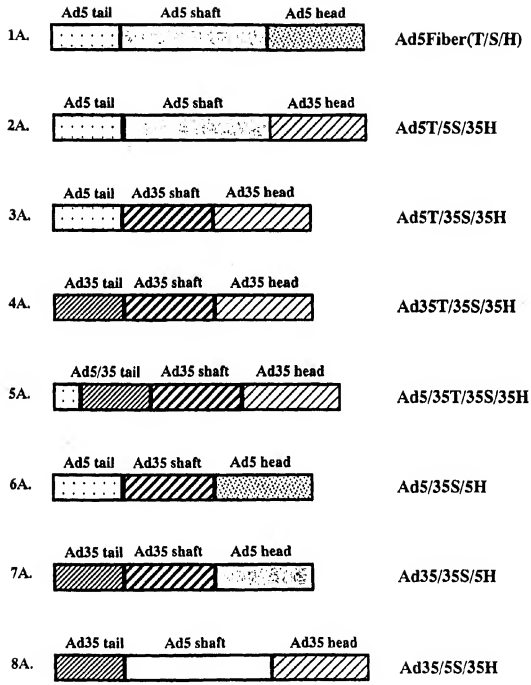
FIGURE 62

FIGURE 63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Ad5 head
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Ad35 shaft
Ad35 head
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Ad35 shaft
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uuuuuuu 7

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<213> Artificial sequence

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<400> 3
uucuucuu 8

<210> 4

<211> 7

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<213> Ebola virus

<400> 4
aaaaaaa 7

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<211> 8

<212> DNA

<213> Artificial sequence

<220>

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<400> 5
aagaagaa 8

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<213> Ebola virus

<400> 6
uuuuuu 6

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<223> Modified RNA editing site

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<223> DNA of modified RNA editing site

<400> 8
ttcttc 6

<210> 9

<211> 21

<212> PRT

<213> Homo sapiens

<400> 9

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1 5 10 15

Asp Phe Met Ser Leu
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Arg Arg Thr Arg Arg
1 5

<210> 11

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<212> PRT

<213> Human immunodeficiency virus type 1

<400> 11

Arg Glu Lys Arg
1

<210> 12

<211> 9

<212> DNA

<213> Artificial sequence

<220>

<223> DNA of GAG site

<400> 12
ggagctggt 9

<210> 13

<211> 3

<212> PRT

<213> Artificial sequence

<220>

<223> GAG site

<400> 13

Gly Ala Gly
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<210> 14

<211> 3157

<212> DNA

<213> Artificial sequence

<220>

<223> Env/Tat/Rev

<400> 14

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa 300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag 420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa 480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc 540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg 600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat 660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc 720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg 780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa 840

aattaacccc actctgtgtt agtttaaagt gcactgattt gaagaatgat actaatacca 900

atagtagtag cgggagaatg ataatggaga aaggagagat aaaaaactgc tctttcaata 960

tcagcacaag cataagaggt aaggtgcaga aagaatatgc atttttttat aaacttgata 1020

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atgtcagcac agtacaatgt acacatggaa ttaggccagt agtatcaact caactgctgt 1260

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ctaaaaccat aatagtacag ctgaaccaat ctgtagaaat taattgtaca agacccaaca 1380

acaatacaag aaaaagtatc cgtatccaga gaggaccagg gagagcattt gttacaatag 1440

gaaaaatagg aaatatgaga caagcacatt gtaacattag tagagcaaaa tggaataaca 1500

ctttaaaaca gatagatagc aaattaagag aacaatttgg aaataataaa acaataatct 1560

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gtactaaagg gtcaaataac actgaaggaa gtgacacaat caccctccca tgcagaataa 1740

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gcaacaatga gtccgagatc ttcagacctg gaggaggaga tatgagggac aattggagaa 1920

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caaagagaag agtggtgcag agagaaaaaa gagcagtggg aataggagct ttgttccttg 2040

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ccagacaatt attgtctggt atagtgcagc agcagaacaa tttgctgagg gctattgagg 2160

cgcaacagca tctgttgcaa ctcacagtct ggggcatcaa gcagctccag gcaagaatcc 2220

tggctgtgga aagataccta aaggatcaac agctcctggg gatttggggt tgctctggaa 2280

aactcatttg caccactgct gtgccttgga atgctagttg gagtaataaa tctctggaac 2340

agatttggaa taacatgacc tggatggagt gggacagaga aattaacaat tacacaagct 2400

taatacactc cttaattgaa gaatcgcaaa accagcaaga aaagaatgaa caagaattat 2460

tggaattaga taaatgggca agtttgtgga attggtttaa cataacaaat tggctgtggt 2520

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ggagcctgtg cctcttcagc taccaccgct tgagagactt actcttgatt gtaacgagga 2820

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agtattggag tcaggagcta aagaatagtg ctgttagctt gctcaatgcc acagctatag 2940

cagtagctga ggggacagat agggttatag aagtagtaca aggagcttat agagctattc 3000

gccacatacc tagaagaata agacagggct tggaaaggat tttgctataa gatgggtggc 3060

aagtggtcaa aaagtagtgt ggttggatgg cctgctgtaa gggaaagaat gagacgagct 3120

gagccagcag cagatggggt gggagcagca tctcgag 3157

<210> 15

<211> 508

<212> DNA

<213> Artificial sequence

<220>

<223> Modified IL-2

<400> 15

tcactctctt taatcactac tcacagtaac ctcaactcct gccacaatgt acaggatgca 60

actcctgtct tgcattgcac taagtcttgc acttgtcaca aacagtgcac ctacttcaag 120

ttctacaaag aaaacacagc tacaactgga gcatttactg ctggatttac agatgatttt 180

gaatggaatt aataattaca agaatcccaa actcaccagg atgctcacat ttaagtttta 240

catgcccaag aaggccacag aactgaaaca tcttcagtgt cttgaagaag aactcaaacc 300

tctggaggaa gtgctaaatt tagctcaaag caaaaacttt cacttaagac ccagggactt 360

aatcagcaat atcaacgtaa tagttctgga actaaaggga tctgaaacaa cattcatgtg 420

tgaatatgct gatgagacag caaccattgt agaatttctg aacagatgga ttacctttttg 480

tcaaagcatc atctcaacac taacttga 508

<210> 16

<211> 2280

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env

<400> 16

gaattcgcca ccatgggagt gaaggagaaa tatcagcact tgtggagatg ggggtggaga 60

tggggcacca tgctccttgg gatgttgatg atctgtagtg ctacagaaaa attgtgggtc 120

acagtctatt atggggtacc tgtgtggaag gaagcaacca ccactctatt ttgtgcatca 180

gatgctaaag catatgatac agaggtacat aatgtttggg ccacacatgc ctgtgtaccc 240

acagacccca acccacaaga agtagtattg gtaaatgtga cagaaaattt taacatgtgg 300

aaaaatgaca tggtagaaca gatgcatgag gatataatca gtttatggga tcaaagccta 360

aagccatgtg taaaattaac cccactctgt gttagtttaa agtgcactga tttgaagaat 420

gatactaata ccaatagtag tagcgggaga atgataatgg agaaaggaga gataaaaaac 480

tgctctttca atatcagcac aagcataaga ggtaaggtgc agaaagaata tgcatttttt 540

tataaacttg atataatacc aatagataat gatactacca gctatacgtt gacaagttgt 600

aacacctcag tcattacaca ggcctgtcca aaggtatcct ttgagccaat tcccatacat 660

tattgtgccc cggctggttt tgcgattcta aaatgtaata ataagacgtt caatggaaca 720

ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca 780

actcaactgc tgttaaatgg cagtctggca gaagaagagg tagtaattag atctgccaat 840

ttcacagaca atgctaaaac cataatagta cagctgaacc aatctgtaga aattaattgt 900

acaagaccca acaacaatac aagaaaaagt atccgtatcc agagaggacc agggagagca 960

tttgttacaa taggaaaaat aggaaatatg agacaagcac attgtaacat tagtagagca 1020

aaatggaata acactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat 1080

aaaacaataa tctttaagca gtcctcagga ggggacccag aaattgtaac gcacagtttt 1140

aattgtggag gggaatttttt ctactgtaat tcaacacaac tgtttaatag tacttggttt 1200

aatagtactt ggagtactaa agggtcaaat aacactgaag gaagtgacac aatcaccctc 1260

ccatgcagaa taaaacaaat tataaacatg tggcaggaag taggaaaagc aatgtatgcc 1320

cctcccatca gtggacaaat tagatgttca tcaaatatta cagggctgct attaacaaga 1380

gatggtggta atagcaacaa tgagtccgag atcttcagac ctggaggagg agatatgagg 1440

gacaattgga gaagtgaatt atataaatat aaagtagtaa aaattgaacc attaggagta 1500

gcacccacca aggcaaagag aagagtggtg cagactagtg cagtgggaat aggagctttg 1560

ttccttgggt tcttgggagc agcaggaagc actatgggcg cagcgtcaat gacgctgacg 1620

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agaatcctgg ctgtggaaag atacctaaag gatcaacagc tcctggggat ttggggttgc 1800

tctggaaaac tcatttgcac cactgctgtg ccttggaatg ctagttggag taataaatct 1860

ctggaacaga tttggaataa catgacctgg atggagtggg acagagaaat taacaattac 1920

acaagcttaa tacactcctt aattgaagaa tcgcaaaacc agcaagaaaa gaatgaacaa 1980

gaattattgg aattagataa atgggcaagt ttgtggaatt ggtttaacat aacaaattgg 2040

ctgtggtata taaaattatt cataatgata gtaggaggct tggtaggttt aagaatagtt 2100

tttgctgtac tttctgtagt gaatagagtt aggcagggat attcaccatt atcgtttcag 2160

acccacctcc caatcccgag gggacccgac aggcccgaag gaatagaaga agaaggtgga 2220

gagagagaca gagacagatc cattcgatta gtgaacggat ccttagcact tatctggtaa 2280

<210> 17

<211> 1496

<212> DNA

<213> Artificial sequence

<220>

<223> Full length Gag

<400> 17

ggctagaagg agagaggatg ggtgcgagag cgtcagtatt aagcggggga gaattagatc 60

gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta aaacatatag 120

tatgggcaag cagggagcta gaacgactac aaccatccct tcagacagga tcagaagaac 180

ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg atagagataa 240

aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt aagaaaaaag 300

cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat taccctatag 360

tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact ttaaatgcat 420

gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg ttttcagcat 480

tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg gggggacatc 540

aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa tgggatagag 600

tacatccagt gcatgcaggg cctattgcac caggccagat gagagaacca aggggaagtg 660

acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca aataatccac 720

ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat aaaatagtaa 780

gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa ccttttagag 840

actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag gaggtaaaaa 900

attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag actattttaa 960

aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag ggagtaggag 1020

gacccggcca taaggcaaga gttttggctg aagcaatgag ccaagtaaca aatacagcta 1080

ccataatgat gcagagaggc aattttagga accaaagaaa gatggttaag tgtttcaatt 1140

gtggcaaaga agggcacaca gccagaaatt gcagggcccc taggaaaaag ggctgttgga 1200

aatgtggaaa ggaaggacac caaatgaaag attgtactga gagacaggct aatttttag 1260

ggaagatctg gccttcctac aagggaaggc cagggaattt tcttcagagc agaccagagc 1320

caacagcccc accatttctt cagagcagac cagagccaac agccccacca gaagagagct 1380

tcaggtctgg ggtagagaca acaactcccc ctcagaagca ggagccgata gacaaggaac 1440

tgtatccttt aacttccctc agatcactct ttggcaacga cccctcgtca caataa 1496

<210> 18

<211> 492

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 18

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Leu Gln Pro Ser Leu
35 40 45

Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr
50 55 60

Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala
65 70 75 80

Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln
85 90 95

Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr
100 105 110

Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser
115 120 125

Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe
130 135 140

Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr
145 150 155 160

Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala
165 170 175

Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp
180 185 190

Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met
195 200 205

Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln
210 215 220

Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu
225 230 235 240

Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met
245 250 255

Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro
260 265 270

Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln
275 280 285

Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln
290 295 300

Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala
305 310 315 320

Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro
325 330 335

Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Val Thr Asn
340 345 350

Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn Gln Arg Lys
355 360 365

Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr Ala Arg Asn
370 375 380

Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
385 390 395 400

His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
405 410 415

Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg
420 425 430

Pro Glu Pro Thr Ala Pro Pro Phe Leu Gln Ser Arg Pro Glu Pro Thr
435 440 445

Ala Pro Pro Glu Glu Ser Phe Arg Ser Gly Val Glu Thr Thr Thr Pro
450 455 460

Pro Gln Lys Gln Glu Pro Ile Asp Lys Glu Leu Tyr Pro Leu Thr Ser
465 470 475 480

Leu Arg Ser Leu Phe Gly Asn Asp Pro Ser Ser Gln
485 490

<210> 19

<211> 2941

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env from HIV strain pNL4-3

<400> 19
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gcgttactcg acagaggaga gcaagaaatg gagccagtag atcctagact agagccctgg 120

aagcatccag gaagtcagcc taaaactgct tgtaccaatt gctattgtaa aaagtgttgc 180

tttcattgcc aagtttgttt catgacaaaa gccttaggca tctcctatgg caggaagaag 240

cggagacagc gacgaagagc tcatcagaac agtcagactc atcaagcttc tctatcaaag 300

cagtaagtag tacatgtaat gcaacctata atagtagcaa tagtagcatt agtagtagca 360

ataataatag caatagttgt gtggtccata gtaatcatag aatataggaa aatattaaga 420

caaagaaaaa tagacaggtt aattgataga ctaatagaaa gagcagaaga cagtggcaat 480

gagagtgaag gagaagtatc agcacttgtg gagatggggg tggaaatggg gcaccatgct 540

ccttgggata ttgatgatct gtagtgctac agaaaaattg tgggtcacag tctattatgg 600

ggtacctgtg tggaaggaag caaccaccac tctattttgt gcatcagatg ctaaagcata 660

tgatacagag gtacataatg tttgggccac acatgcctgt gtacccacag accccaaccc 720

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agaacagatg catgaggata taatcagttt atgggatcaa agcctaaagc catgtgtaaa 840

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gggacgcagg gggtgggaag ccctcaaata ttggtggaat ctcctacagt attggagtca 2880

ggaactaaag aatagtgctg ttaacttgct caatgccaca gccatagcag tagctgagta 2940

a 2941

<210> 20

<211> 2746

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev from pNL4-3

<400> 20

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gcgttactcg acagaggaga gcaagaaatg gagccagtag atcctagact agagccctgg 120

aagcatccag gaagtcagcc taaaactgct tgtaccaatt gctattgtaa aaagtgttgc 180

tttcattgcc aagtttgttt catgacaaaa gccttaggca tctcctatgg caggaagaag 240

cggagacagc gacgaagagc tcatcagaac agtcagactc atcaagcttc tctatcaaag 300

cagtaagtag tacatgtaat gcaacctata atagtagcaa tagtagcatt agtagtagca 360

ataataatag caatagttgt gtggtccata gtaatcatag aatataggaa aatattaaga 420

caaagaaaaa tagacaggtt aattgataga ctaatagaaa gagcagaaga cagtggcaat 480

gagagtgaag gagaagtatc agcacttgtg gagatggggg tggaaatggg gcaccatgct 540

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acaagaagta gtattggtaa atgtgacaga aaatttaac atgtggaaaa atgacatggt 780

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gaacacatct gtagaaatta attgtacaag acccaacaac aatacaagaa aaagtatccg 1200

tatccagagg ggaccaggga gagcatttgt tacaatagga aaaataggaa atatgagaca 1260

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<210> 21
<211> 3417
<212> DNA
<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev/Nef from strain BH10

<400> 21

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ggcgttactc gacagaggag agcaagaaat ggagccagta gatcctagac tagagccctg 120

gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa 300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360

aataatagta gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag 420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa 480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc 540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg 600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat 660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc 720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg 780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa 840

aattaacccc actctgtgtt agtttaaagt gcactgattt gaagaatgat actaatacca 900

atagtagtag cgggagaatg ataatggaga aaggagagat aaaaaactgc tctttcaata 960

tcagcacaag cataagaggt aaggtgcaga aagaatatgc atttttttat aaacttgata 1020

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atgtcagcac agtacaatgt acacatggaa ttaggccagt agtatcaact caactgctgt 1260

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ctaaaaccat aatagtacag ctgaaccaat ctgtagaaat taattgtaca agacccaaca 1380

acaatacaag aaaaagtatc cgtatccaga gaggaccagg gagagcattt gttacaatag 1440

gaaaaatagg aaatatgaga caagcacatt gtaacattag tagagcaaaa tggaataaca 1500

ctttaaaaca gatagatagc aaattaagag aacaatttgg aaataataaa acaataatct 1560

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<210> 22
<211> 2950
<212> DNA
<213> Artificial sequence

Genphar.740.ST25.txt

<220>

<223> Modified Env/Nef from strain BH10

<400> 22

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tggggcacca tgctccttgg gatgttgatg atctgtagtg ctacagaaaa attgtgggtc 120

acagtctatt atggggtacc tgtgtggaag gaagcaacca ccactctatt ttgtgcatca 180

gatgctaaag catatgatac agaggtacat aatgtttggg ccacacatgc ctgtgtaccc 240

acagacccca acccacaaga agtagtattg gtaaatgtga cagaaaattt taacatgtgg 300

aaaaatgaca tggtagaaca gatgcatgag gatataatca gtttatggga tcaaagccta 360

aagccatgtg taaaattaac cccactctgt gttagtttaa agtgcactga tttgaagaat 420

gatactaata ccaatagtag tagcgggaga atgataatgg agaaaggaga gataaaaaac 480

tgctctttca atatcagcac aagcataaga ggtaaggtgc agaaagaata tgcatttttt 540

tataaacttg atataatacc aatagataat gatactacca gctatacgtt gacaagttgt 600

aacacctcag tcattacaca ggcctgtcca aaggtatcct ttgagccaat tcccatacat 660

tattgtgccc cggctggttt tgcgattcta aaatgtaata ataagacgtt caatggaaca 720

ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca 780

actcaactgc tgttaaatgg cagtctggca gaagaagagg tagtaattag atctgccaat 840

ttcacagaca atgctaaaac cataatagta cagctgaacc aatctgtaga aattaattgt 900

acaagaccca acaacaatac aagaaaaagt atccgtatcc agagaggacc agggagagca 960

tttgttacaa taggaaaaat aggaaatatg agacaagcac attgtaacat tagtagagca 1020

aaatggaata acactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat 1080

aaaacaataa tctttaagca gtcctcagga ggggacccag aaattgtaac gcacagtttt 1140

aattgtggag gggaattttt ctactgtaat tcaacacaac tgtttaatag tacttggttt 1200

aatagtactt ggagtactaa agggtcaaat aacactgaag gaagtgacac aatcaccctc 1260

ccatgcagaa taaaacaaat tataaacatg tggcaggaag taggaaaagc aatgtatgcc 1320

cctcccatca gtggacaaat tagatgttca tcaaatatta cagggctgct attaacaaga 1380

gatggtggta atagcaacaa tgagtccgag atcttcagac ctggaggagg agatatgagg 1440

gacaattgga gaagtgaatt atataaatat aaagtagtaa aaattgaacc attaggagta 1500

gcacccacca aggcaaagag aagagtggtg cagactagtg cagtgggaat aggagctttg 1560

ttccttgggt tcttgggagc agcaggaagc actatgggcg cagcgtcaat gacgctgacg 1620

gtacaggcca gacaattatt gtctggtata gtgcagcagc agaacaattt gctgagggct 1680

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caaggcagct gtagatctta gccacttttt aaaagaaaag gggggactgg aagggctaat 2880
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ccctgattag 2950

<210> 23
<211> 2747
<212> DNA
<213> Artificial sequence

<220>
<223> Modified Env/Tat from strain BH10

<400> 23
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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa 300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360

aataataata gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag 420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa 480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc 540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg 600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat 660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc 720

cacaagaagt agtattggta aatgtgacag aaaatttaa catgtggaaa aatgacatgg 780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa 840

aattaacccc actctgtgtt agtttaaagt gcactgattt gaagaatgat actaatacca 900

atagtagtag cgggagaatg ataatggaga aaggagagat aaaaaactgc tctttcaata 960

tcagcacaag cataagaggt aaggtgcaga aagaatatgc attttttat aaacttgata 1020

taataccaat agataatgat actaccagct atacgttgac aagttgtaac acctcagtca 1080

ttacacaggc ctgtccaaag gtatcctttg agccaattcc catacattat tgtgccccgg 1140

ctggttttgc gattctaaaa tgtaataata agacgttcaa tggaacagga ccatgtacaa 1200

atgtcagcac agtacaatgt acacatggaa ttaggccagt agtatcaact caactgctgt 1260

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ctaaaaccat aatagtacag ctgaaccaat ctgtagaaat taattgtaca agacccaaca 1380

acaatacaag aaaaagtatc cgtatccaga gaggaccagg gagagcattt gttacaatag 1440

gaaaaatagg aaatatgaga caagcacatt gtaacattag tagagcaaaa tggaataaca 1500

ctttaaaaca gatagatagc aaattaagag aacaatttgg aaataataaa acaataatct 1560

ttaagcagtc ctcaggaggg gacccagaaa ttgtaacgca cagttttaat tgtggagggg 1620

aatttttcta ctgtaattca acacaactgt ttaatagtac ttggtttaat agtacttgga 1680

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aacaaattat aaacatgtgg caggaagtag gaaaagcaat gtatgcccct cccatcagtg 1800

gacaaattag atgttcatca aatattacag ggctgctatt aacaagagat ggtggtaata 1860

gcaacaatga gtccgagatc ttcagacctg gaggaggaga tatgagggac aattggagaa 1920

gtgaattata taaatataaa gtagtaaaaa ttgaaccatt aggagtagca cccaccaagg 1980

caaagagaag agtggtgcag actagtgcag tgggaatagg agctttgttc cttgggttct 2040

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ggaataacat gacctggatg gagtgggaca gagaaattaa caattacaca agcttaatac 2400

actccttaat tgaagaatcg caaaaccagc aagaaaagaa tgaacaagaa ttattggaat 2460

tagataaatg ggcaagtttg tggaattggt ttaacataac aaattggctg tggtatataa 2520

aattattcat aatgatagta ggaggcttgg taggtttaag aatagttttt gctgtacttt 2580

ctgtagtgaa tagagttagg cagggatatt caccattatc gtttcagacc cacctcccaa 2640

tcccgagggg acccgacagg cccgaaggaa tagaagaaga aggtggagag agagacagag 2700

acagatccat tcgattagtg aacggatcct tagcacttat ctggtaa 2747

<210> 24

<211> 2583

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env

<400> 24

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acagtctatt atggggtacc tgtgtggaag gaagcaacca ccactctatt ttgtgcatca 180

gatgctaaag catatgatac agaggtacat aatgtttggg ccacacatgc ctgtgtaccc 240

acagacccca acccacaaga agtagtattg gtaaatgtga cagaaaattt taacatgtgg 300

aaaaatgaca tggtagaaca gatgcatgag gatataatca gtttatggga tcaaagccta 360

aagccatgtg taaaattaac cccactctgt gttagtttaa agtgcactga tttgaagaat 420

gatactaata ccaatagtag tagcgggaga atgataatgg agaaaggaga gataaaaaac 480

tgctctttca atatcagcac aagcataaga ggtaaggtgc agaaagaata tgcatttttt 540

tataaacttg atataatacc aatagataat gatactacca gctatacgtt gacaagttgt 600

aacaccttcag tcattacaca ggcctgtcca aaggtatcct ttgagccaat tcccatacat 660

tattgtgccc cggctggttt tgcgattcta aaatgtaata ataagacgtt caatggaaca 720

ggaccatgta caaatgtcag cacagtacaa tgtacacatg gaattaggcc agtagtatca 780

actcaactgc tgttaaatgg cagtctggca gaagaagagg tagtaattag atctgccaat 840

ttcacagaca atgctaaaac cataatagta cagctgaacc aatctgtaga aattaattgt 900

acaagaccca acaacaatac aagaaaaagt atccgtatcc agagaggacc agggagagca 960

tttgttacaa taggaaaaat aggaaatatg agacaagcac attgtaacat tagtagagca 1020

aaatggaata acactttaaa acagatagat agcaaattaa gagaacaatt tggaaataat 1080

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aattgtggag gggaattttt ctactgtaat tcaacacaac tgtttaatag tacttggttt 1200

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cctcccatca gtggacaaat tagatgttca tcaaatatta cagggctgct attaacaaga 1380

gatggtggta atagcaacaa tgagtccgag atcttcagac ctggaggagg agatatgagg 1440

gacaattgga gaagtgaatt atataaatat aaagtagtaa aaattgaacc attaggagta 1500

gcacccacca aggcaaagag aagagtggtg cagagagaaa aaagagcagt gggaatagga 1560

gctttgttcc ttgggttctt gggagcagca ggaagcacta tgggcgcagc gtcaatgacg 1620

ctgacggtac aggccagaca attattgtct ggtatagtgc agcagcagaa caatttgctg 1680

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gaacaagaat tattggaatt agataaatgg gcaagtttgt ggaattggtt taacataaca 2040

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taa 2583

<210> 25

<211> 108

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 25
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gcatttgtta caataggaaa aataggaaat atgagacaag cacattgt 108

<210> 26

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 26
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tatgcaacag gtgatataat aggggatata agacaagcac attgt 105

<210> 27

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 27
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tatgcaacag gagaaataat aggagatata agacaagcac attgt 105

<210> 28

<211> 102

<212> DNA

<213> Human immunodeficiency virus type 1

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tatacaacaa gaagaataga agatataaga agagcacatt gt 102

<210> 29

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

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tatagaacag gagacataac aggagatata agaaaagcat attgt 105

<210> 30

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 30
tgtacaagac ccaacaacaa tacaagaaaa agaatatctt taggaccagg acgagtattt 60

tatacagcag gagaaataat aggagacatc agaaaggcac attgt 105

<210> 31

<211> 105

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 31
tgtaccagac ctaataacaa tacaagaaaa agtataactt ttgcaccagg acaagcgctc 60

tatgcaacag gtgaaataat aggagatata agacaagcac attgt 105

<210> 32

<211> 2562

<212> DNA

<213> Artificial sequence

Genphar.740.ST25.txt

<220>

<223> Env with multi-clade V3 loops

<400> 32

atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60

ctccttggga tgttgatgat ctgtagtgct acagaaaaat tgtgggtcac agtctattat 120

ggggtacctg tgtggaagga agcaaccacc actctatttt gtgcatcaga tgctaaagca 180

tatgatacag aggtacataa tgtttgggcc acacatgcct gtgtacccac agaccccaac 240

ccacaagaag tagtattggt aaatgtgaca gaaaatttta acatgtggaa aaatgacatg 300

gtagaacaga tgcatgagga tataatcagt ttatgggatc aaagcctaaa gccatgtgta 360

aaattaaccc cactctgtgt tggagctggt agttgtaaca cctcagtcat tacacaggcc 420

tgtccaaagg tatcctttga gccaattccc atacattatt gtgccccggc tggttttgcg 480

attctaaaat gtaataataa gacgttcaat ggaacaggac catgtacaaa tgtcagcaca 540

gtacaatgta cacatggaat taggccagta gtatcaactc aactgctgtt aaatggcagt 600

ctggcagaag aagaggtagt aattagatct gccaatttca cagacaatgc taaaaccata 660

atagtacagc tgaaccaatc tgtagaaatt aattgtacaa gacccaacaa caatacaaga 720

aaaagtatcc gtatccagag aggaccaggg agagcatttg ttacaatagg aaaaatagga 780

aatatgagac aagcacattg tctcgggtgt accagaccta acaacaatac aagaaaaagt 840

gtacgtatag gaccaggaca aacattctat gcaacaggtg atataatagg ggatataaga 900

caagcacatt gttgtacgag acccaacaat aatacaagaa aaagtataag gataggacca 960

ggacaagcat tctatgcaac aggagaaata ataggagata taagacaagc acattgttgc 1020

acaaggccct acaacaatat aagacaaagg acccccatag gactagggca agcactctat 1080

acaacaagaa gaatagaaga tataagaaga gcacattgtt gtaccagacc ctccaccaat 1140

acaagaacaa gtatacgtat aggaccagga caagtattct atagaacagg agacataaca 1200

ggagatataa gaaaagcata ttgtggatcc tgtacaagac ccaacaacaa tacaagaaaa 1260

agaatatctt taggaccagg acgagtattt tatacagcag gagaaataat aggagacatc 1320

agaaaggcac attgttgtac cagacctaat aacaatacaa gaaaaagtat aacttttgca 1380

ccaggacaag cgctctatgc aacaggtgaa ataataggag atataagaca agcacattgt 1440

ctcgggaaca ttagtagagc aaaatggaat aacactttaa aacagataga tagcaaatta 1500

agagaacaat ttggaaataa taaaacaata atctttaagc agtcctcagg aggggaccca 1560

gaaattgtaa cgcacagttt taattgtgga ggggaatttt tctactgtaa ttcaacacaa 1620

ctgtttaata gtacttggtt taatagtact tggagtacta aagggtcaaa taacactgaa 1680

ggaagtgaca caatcaccct cccatgcaga ataaaacaaa ttataaacat gtggcaggaa 1740

gtaggaaaag caatgtatgc ccctcccatc agtggacaaa ttagatgttc atcaaatatt 1800

acagggctgc tattaacaag agatggtggt aatagcaaca atgagtccga gatcttcaga 1860

cctggaggag gagatatgag ggacaattgg agaagtgaat tatataaata taaagtagta 1920

aaaattgaac cattaggagt agcacccacc aaggcaaaga gaagagtggt gcagactagt 1980

gcagtgggaa taggagcttt gttccttggg ttcttgggag cagcaggaag cactatgggc 2040

gcagcgtcaa tgacgctgac ggtacaggcc agacaattat tgtctggtat agtgcagcag 2100

cagaacaatt tgctgagggc tattgaggcg caacagcatc tgttgcaact cacagtctgg 2160

ggcatcaagc agctccaggc aagaatcctg gctgtggaaa gatacctaaa ggatcaacag 2220

ctcctgggga tttggggttg ctctggaaaa ctcatttgca ccactgctgt gccttggaat 2280

gctagttgga gtaataaatc tctggaacag atttggaata acatgacctg gatggagtgg 2340

gacagagaaa ttaacaatta cacaagctta atacactcct taattgaaga atcgcaaaac 2400

cagcaagaaa agaatgaaca agaattattg gaattagata aatgggcaag tttgtggaat 2460

tggtttaaca taacaaattg gctgtggtat ataaaatcgt ggctgctgct gctcctgctc 2520

tccctctccc tcctccaggc cacggatttc atgtccctgt ga 2562

<210> 33

<211> 853

<212> PRT

<213> Artificial sequence

<220>

<223> Modified Env with multi-clade V3 loops

<400> 33

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
115 120 125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
245 250 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
260 265 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
275 280 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
290 295 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
305 310 315 320

Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln
325 330 335

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
340 345 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
355 360 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
370 375 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385 390 395 400

Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn
405 410 415

Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr
420 425 430

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
435 440 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile
485 490 495

Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe
500 505 510

Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn
515 520 525

Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser
530 535 540

Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly Ser Asn Asn Thr Glu
545 550 555 560

Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
565 570 575

Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly
580 585 590

Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
595 600 605

Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Pro Gly Gly Gly
610 615 620

Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val
625 630 635 640

Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val
645 650 655

Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu
660 665 670

Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val
675 680 685

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
690 695 700

Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
705 710 715 720

Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
725 730 735

Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
740 745 750

Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
755 760 765

Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
770 775 780

Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
785 790 795 800

Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
805 810 815

Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys

820 825 830

Ser Trp Leu Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr
835 840 845

Asp Phe Met Ser Leu
850

<210> 34

<211> 1092

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 34

atgggtgcga gagcgtcagt attaagcggg ggagaattag atcgatggga aaaaattcgg 60

ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag 120

ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180

ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240

acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300

ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360

gacacaggac acagcagtca ggtcagccaa aattacccta tagtgcagaa catccagggg 420

caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480

gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc 540

ccacaagatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg 600

ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtacatcc agtgcatgca 660

gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720

agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa 780

atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc 840

agcattctgg acataagaca aggaccaaaa gaacctttta gagactatgt agaccggttc 900

tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc 960

ttgttggtcc aaaatgcgaa cccagattgt aagactattt taaaagcatt gggaccagcg 1020

gctacactag aagaaatgat gacagcatgt cagggagtag gaggacccgg ccataaggca 1080

agagttttgt aa 1092

<210> 35

<211> 1179

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 35
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60
ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcgggggga 120
gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180
aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240
gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300
tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg 360
atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420
aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480
taccctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact 540
ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg 600
ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg 660
gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa 720
tgggatagag tcatccagt gcatgcaggg cctattgcac caggccagat gagagaacca 780
aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca 840
aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat 900
aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa 960
ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag 1020
gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag 1080
actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag 1140
ggagtaggag gacccggcca taaggcaaga gttttgtaa 1179

<210> 36

<211> 1308

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 36
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60

ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga 120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300

tcagaagaac ttagatcatt atataatACa gtagcaaccc tctattgtgt gcatcaaagg 360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480

taccctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact 540

ttaaatgcat gggtaaaagt agtagaagag aaggctttca gcccagaagt aatacccatg 600

ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg 660

gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa 720

tgggatagag tcatccagt gcatgcaggg cctattgcac caggccagat gagagaacca 780

aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca 840

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat 900

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa 960

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag 1020

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag 1080

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag 1140

ggagtaggag gacccggcca taaggcaaga gttttgttat tcataatgat agtaggaggc 1200

ttggtaggtt taagaatagt ttttgctgta ctttctgtag tgaatagagt taggcaggga 1260

tattcaccat tatcgtttca gacccacctc ccaatcccga ggggataa 1308

<210> 37

<211> 363

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 37

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
355 360

<210> 38

<211> 410

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 38

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65 70 75 80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
85 90 95

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala
100 105 110

Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu
115 120 125

Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala
130 135 140

Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn
145 150 155 160

Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165 170 175

Gln Asn Tyr Pro Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln
180 185 190

Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val
195 200 205

His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val
210 215 220

Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu
225 230 235 240

Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val
245 250 255

Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu
260 265 270

Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile
275 280 285

Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr
290 295 300

Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro
305 310 315 320

Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn
325 330 335

Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln
340 345 350

Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr
355 360 365

Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Thr Ile Leu Lys Ala Leu

370 375 380

Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
385 390 395 400

Gly Gly Pro Gly His Lys Ala Arg Val Leu
405 410

<210> 39

<211> 453

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 39

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu
50 55 60

Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His
65 70 75 80

Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly
85 90 95

Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln
100 105 110

Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr
115 120 125

Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr
130 135 140

Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys
145 150 155 160

Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165 170 175

Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln
180 185 190

Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu
195 200 205

Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
210 215 220

Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
225 230 235 240

His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala
245 250 255

Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro
260 265 270

Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
275 280 285

Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
290 295 300

Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
305 310 315 320

Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
325 330 335

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
340 345 350

Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
355 360 365

Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu
370 375 380

Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val
385 390 395 400

Gly Gly Pro Gly His Lys Ala Arg Val Leu Leu Phe Ile Met Ile Val
405 410 415

Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Val Val
420 425 430

Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu
435 440 445

Pro Ile Pro Arg Gly
450

<210> 40

<211> 399

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 40
atgggtgcga gagcgtcagt attaagcggg ggagaattag atcgatggga aaaaattcgg 60

ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag 120

ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180

ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240

acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct 300

ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct 360

gacacaggac acagcagtca ggtcagccaa aattactaa 399

<210> 41

<211> 486

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 41
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60

ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcggggga 120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300

tcagaagaac ttagatcatt atataataca gtagcaaccc tctattgtgt gcatcaaagg 360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480

tactaa 486

<210> 42

<211> 615

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 42

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ctccttggga tgttgatgat ctgtagtgct ggtgcgagag cgtcagtatt aagcgggggga 120

gaattagatc gatgggaaaa aattcggtta aggccagggg gaaagaaaaa atataaatta 180

aaacatatag tatgggcaag cagggagcta gaacgattcg cagttaatcc tggcctgtta 240

gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 300

tcagaagaac ttagatcatt atataatаca gtagcaaccc tctattgtgt gcatcaaagg 360

atagagataa aagacaccaa ggaagcttta gacaagatag aggaagagca aaacaaaagt 420

aagaaaaaag cacagcaagc agcagctgac acaggacaca gcagtcaggt cagccaaaat 480

tacttattca taatgatagt aggaggcttg gtaggtttaa gaatagtttt tgctgtactt 540

tctgtagtga atagagttag gcagggatat tcaccattat cgtttcagac ccacctccca 600

atcccgaggg gataa 615

<210> 43

<211> 132

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 43

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
115 120 125

Ser Gln Asn Tyr
130

<210> 44

<211> 179

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 44

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu
65 70 75 80

Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu Gln Pro Ser
85 90 95

Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Gly Gln Leu Gln
100 105 110

Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr
115 120 125

Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr
130 135 140

Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys
145 150 155 160

Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser
165 170 175

Gln Asn Tyr

<210> 45

<211> 186

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 45

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Gly Ala
20 25 30

Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp Glu Lys Ile
35 40 45

Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys His Ile Val
50 55 60

Trp Ala Ser Arg Glu Leu Glu Arg Gly Gln Leu Gln Pro Ser Leu Gln
65 70 75 80

Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu
85 90 95

Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu
100 105 110

Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln

115 120 125

Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val Ser Gln Asn Tyr Leu
130 135 140

Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala
145 150 155 160

Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser
165 170 175

Phe Gln Thr His Leu Pro Ile Pro Arg Gly
180 185

<210> 46

<211> 699

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 46

atgcctatag tgcagaacat ccaggggcaa atggtacatc aggccatatc acctagaact 60

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ttttcagcat tatcagaagg agccacccca caagatttaa acaccatgct aaacacagtg 180

gggggacatc aagcagccat gcaaatgtta aaagagacca tcaatgagga agctgcagaa 240

tgggatagag tcatccagt gcatgcaggg cctattgcac caggccagat gagagaacca 300

aggggaagtg acatagcagg aactactagt acccttcagg aacaaatagg atggatgaca 360

aataatccac ctatcccagt aggagaaatt tataaaagat ggataatcct gggattaaat 420

aaaatagtaa gaatgtatag ccctaccagc attctggaca taagacaagg accaaaagaa 480

ccttttagag actatgtaga ccggttctat aaaactctaa gagccgagca agcttcacag 540

gaggtaaaaa attggatgac agaaaccttg ttggtccaaa atgcgaaccc agattgtaag 600

actattttaa aagcattggg accagcggct acactagaag aaatgatgac agcatgtcag 660

ggagtaggag gacccggcca taaggcaaga gttttgtaa 699

<210> 47

<211> 786

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 47
atgagagtga aggagaaata tcagcacttg tggagatggg ggtggagatg gggcaccatg 60
ctccttggga tgttgatgat ctgtagtgct cctatagtgc agaacatcca ggggcaaatg 120
gtacatcagg ccatatcacc tagaacttta aatgcatggg taaaagtagt agaagagaag 180
gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc caccccacaa 240
gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa 300
gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct 360
attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc 420
cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat 480
aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt 540
ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa 600
actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga aaccttgttg 660
gtccaaaatg cgaacccaga ttgtaagact attttaaaag cattgggacc agcggctaca 720
ctagaagaaa tgatgacagc atgtcaggga gtaggaggac ccggccataa ggcaagagtt 780
ttgtaa 786

<210> 48
<211> 915
<212> DNA
<213> Human immunodeficiency virus type 1

<400> 48
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ctccttggga tgttgatgat ctgtagtgct cctatagtgc agaacatcca ggggcaaatg 120
gtacatcagg ccatatcacc tagaacttta aatgcatggg taaaagtagt agaagagaag 180
gctttcagcc cagaagtaat acccatgttt tcagcattat cagaaggagc caccccacaa 240
gatttaaaca ccatgctaaa cacagtgggg ggacatcaag cagccatgca aatgttaaaa 300
gagaccatca atgaggaagc tgcagaatgg gatagagtac atccagtgca tgcagggcct 360
attgcaccag gccagatgag agaaccaagg ggaagtgaca tagcaggaac tactagtacc 420
cttcaggaac aaataggatg gatgacaaat aatccaccta tcccagtagg agaaatttat 480
aaaagatgga taatcctggg attaaataaa atagtaagaa tgtatagccc taccagcatt 540
ctggacataa gacaaggacc aaaagaacct tttagagact atgtagaccg gttctataaa 600

actctaagag ccgagcaagc ttcacaggag gtaaaaaatt ggatgacaga aaccttgttg 660

gtccaaaatg cgaacccaga ttgtaagact attttaaaag cattgggacc agcggctaca 720

ctagaagaaa tgatgacagc atgtcaggga gtaggaggac ccggccataa ggcaagagtt 780

ttgttattca taatgatagt aggaggcttg gtaggtttaa gaatagtttt tgctgtactt 840

tctgtagtga atagagttag gcagggatat tcaccattat cgtttcagac ccacctccca 900

atcccgaggg gataa 915

<210> 49

<211> 232

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 49

Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile
1 5 10 15

Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala
20 25 30

Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala
35 40 45

Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
50 55 60

Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu
65 70 75 80

Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
85 90 95

Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
100 105 110

Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly
115 120 125

Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
130 135 140

Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
145 150 155 160

Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu
165 170 175

Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val
180 185 190

Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro
195 200 205

Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
210 215 220

Pro Gly His Lys Ala Arg Val Leu
225 230

<210> 50

<211> 261

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 50

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
20 25 30

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
50 55 60

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65 70 75 80

Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
85 90 95

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg
100 105 110

Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu

115 120 125

Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln
130 135 140

Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr
145 150 155 160

Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser
165 170 175

Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg
180 185 190

Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser
195 200 205

Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala
210 215 220

Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr
225 230 235 240

Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His
245 250 255

Lys Ala Arg Val Leu
260

<210> 51

<211> 286

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 51

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Pro Ile
20 25 30

Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg
35 40 45

Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro
50 55 60

Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln
65 70 75 80

Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met
85 90 95

Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Arg Glu Pro Arg
100 105 110

Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly
115 120 125

Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg
130 135 140

Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr
145 150 155 160

Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr
165 170 175

Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu
180 185 190

Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro
195 200 205

Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu
210 215 220

Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala
225 230 235 240

Arg Val Leu Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg
245 250 255

Ile Val Phe Ala Val Leu Ser Val Val Asn Arg Val Arg Gln Gly Tyr
260 265 270

Ser Pro Leu Ser Phe Gln Thr His Leu Pro Ile Pro Arg Gly
275 280 285

<210> 52

<211> 3839

Genphar.740.ST25.txt

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env/Tat

<400> 52

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

ctttcattgc caagtttgtt tcataacaaa agccttaggc atctcctatg gcaggaagaa 240

gcggagacag cgacgaagac ctcctcaagg cagtcagact catcaagttt ctctatcaaa 300

gcagtaagta gtacatgtaa tgcaacctat acaaatagca atagtagcat tagtagtagc 360

aataatagta gcaatagttg tgtggtccat agtaatcata gaatatagga aaatattaag 420

acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa 480

tgagagtgaa ggagaaatat cagcacttgt ggagatgggg gtggagatgg ggcaccatgc 540

tccttgggat gttgatgatc tgtagtgcta cagaaaaatt gtgggtcaca gtctattatg 600

gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat 660

atgatacaga ggtacataat gtttgggcca cacatgcctg tgtacccaca gaccccaacc 720

cacaagaagt agtattggta aatgtgacag aaaattttaa catgtggaaa aatgacatgg 780

tagaacagat gcatgaggat ataatcagtt tatgggatca aagcctaaag ccatgtgtaa 840

aattaacccc actctgtgtt ggagctggta gttgtaacac ctcagtcatt acacaggcct 900

gtccaaaggt atcctttgag ccaattccca tacattattg tgccccggct ggttttgcga 960

ttctaaaatg taataataag acgttcaatg gaacaggacc atgtacaaat gtcagcacag 1020

tacaatgtac acatggaatt aggccagtag tatcaactca actgctgtta aatggcagtc 1080

tggcagaaga agaggtagta attagatctg ccaatttcac agacaatgct aaaaccataa 1140

tagtacagct gaaccaatct gtagaaatta attgtacaag acccaacaac aatacaagaa 1200

aaagtatccg tatccagaga ggaccaggga gagcatttgt tacaatagga aaaataggaa 1260

atatgagaca agcacattgt ctcgggtgta ccagacctaa caacaataca agaaaaagtg 1320

tacgtatagg accaggacaa acattctatg caacaggtga tataataggg gatataagac 1380

aagcacattg ttgtacgaga cccaacaata atacaagaaa aagtataagg ataggaccag 1440

gacaagcatt ctatgcaaca ggagaaataa taggagatat aagacaagca cattgttgca 1500

caaggcccta caacaatata agacaaagga cccccatagg actagggcaa gcactctata 1560

caacaagaag aatagaagat ataagaagag cacattgttg taccagaccc tccaccaata 1620
caagaacaag tatacgtata ggaccaggac aagtattcta tagaacagga gacataacag 1680
gagatataag aaaagcatat tgtggatcct gtacaagacc caacaacaat acaagaaaaa 1740
gaatatcttt aggaccagga cgagtatttt atacagcagg agaaataata ggagacatca 1800
gaaaggcaca ttgttgtacc agacctaata acaatacaag aaaaagtata acttttgcac 1860
caggacaagc gctctatgca acaggtgaaa taataggaga tataagacaa gcacattgtc 1920
tcgggtgtac cagacctaac aacaatacaa gaaaaagtgt acgtatagga ccaggacaaa 1980
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ccaacaataa tacaagaaaa agtataagga taggaccagg acaagcattc tatgcaacag 2100
gagaaataat aggagatata agacaagcac attgttgcac aaggccctac aacaatataa 2160
gacaaaggac ccccatagga ctagggcaag cactctatac aacaagaaga atagaagata 2220
taagaagagc acattgttgt accagaccct ccaccaatac aagaacaagt atacgtatag 2280
gaccaggaca agtattctat agaacaggag acataacagg agatataaga aaagcatatt 2340
gtggatcctg tacaagaccc aacaacaata caagaaaaag aatatcttta ggaccaggac 2400
gagtatttta tacagcagga gaaataatag gagacatcag aaaggcacat tgttgtacca 2460
gacctaataa caatacaaga aaaagtataa cttttgcacc aggacaagcg ctctatgcaa 2520
caggtgaaat aataggagat ataagacaag cacattgtct cgggaacatt agtagagcaa 2580
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ctcccatcag tggacaaatt agatgttcat caaatattac agggctgcta ttaacaagag 2940
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acaattggag aagtgaatta tataaatata aagtagtaaa aattgaacca ttaggagtag 3060
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tccttgggtt cttgggagca gcaggaagca ctatgggcgc agcgtcaatg acgctgacgg 3180
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tggaacagat ttggaataac atgacctgga tggagtggga cagagaaatt aacaattaca 3480

caagcttaat acactcctta attgaagaat cgcaaaacca gcaagaaaag aatgaacaag 3540

aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata acaaattggc 3600

tgtggtatat aaaattattc ataatgatag taggaggctt ggtaggttta agaatagttt 3660

ttgctgtact ttctgtagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga 3720

cccacctccc aatcccgagg ggacccgaca ggcccgaagg aatagaagaa gaaggtggag 3780

agagagacag agacagatcc attcgattag tgaacggatc cttagcactt atctggtaa 3839

<210> 53

<211> 1101

<212> PRT

<213> Artificial sequence

<220>

<223> Modified Env/Tat

<400> 53

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Arg
1 5 10 15

Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Thr Glu
20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
115 120 125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
245 250 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
260 265 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
275 280 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
290 295 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
305 310 315 320

Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln
325 330 335

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
340 345 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
355 360 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
370 375 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385 390 395 400

Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn
405 410 415

Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr
420 425 430

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
435 440 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
485 490 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
500 505 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
515 520 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
530 535 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545 550 555 560

Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg
565 570 575

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
580 585 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
595 600 605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
610 615 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625 630 635 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
645 650 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
660 665 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
675 680 685

Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
690 695 700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705 710 715 720

Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
725 730 735

Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
740 745 750

Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly
755 760 765

Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
770 775 780

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
785 790 795 800

Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
805 810 815

Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
820 825 830

Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
835 840 845

Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
850 855 860

Ala Lys Arg Arg Val Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu
865 870 875 880

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser

885 890 895

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln
900 905 910

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
915 920 925

Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
930 935 940

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
945 950 955 960

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
965 970 975

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
980 985 990

Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile
995 1000 1005

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu
1010 1015 1020

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
1025 1030 1035

Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile Val Gly Gly
1040 1045 1050

Leu Val Gly Leu Arg Ile Val Phe Ala Thr His Leu Pro Ile Pro
1055 1060 1065

Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu Gly Gly Glu
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Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly Ser Leu Ala
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Leu Ile Trp
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<210> 54

<211> 4040

<212> DNA

<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev

<400> 54

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gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat tgctattgta aaaagtgttg 180

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acaaagaaaa atagacaggt taattgatag actaatagaa agagcagaag acagtggcaa 480

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gggtacctgt gtggaaggaa gcaaccacca ctctattttg tgcatcagat gctaaagcat 660

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ttctaaaatg taataataag acgttcaatg gaacaggacc atgtacaaat gtcagcacag 1020

tacaatgtac acatggaatt aggccagtag tatcaactca actgctgtta aatggcagtc 1080

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aaagtatccg tatccagaga ggaccaggga gagcatttgt tacaatagga aaaataggaa 1260

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tacgtatagg accaggacaa acattctatg caacaggtga tataataggg gatataagac 1380

aagcacattg ttgtacgaga cccaacaata atacaagaaa aagtataagg ataggaccag 1440

gacaagcatt ctatgcaaca ggagaaataa taggagatat aagacaagca cattgttgca 1500

caaggcccta caacaatata agacaaagga cccccatagg actagggcaa gcactctata 1560

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tgtggtatat aaaattattc ataatgatag taggaggctt ggtaggttta agaatagttt 3660

ttgctgtact ttctatagtg aatagagtta ggcagggata ttcaccatta tcgtttcaga 3720

cccacctccc aatcccgagg ggacccgaca ggcccgaagg aatagaagaa gaaggtggag 3780

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atctgcggag cctgtgcctc ttcagctacc accgcttgag agacttactc ttgattgtaa 3900

cgaggattgt ggaacttctg ggacgcaggg ggtgggaagc cctcaaatat tggtggaatc 3960

tcctacagta ttggagtcag gaactaaaga atagtgctgt taacttgctc aatgccacag 4020

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<210> 55

<211> 1186

<212> PRT

<213> Artificial sequence

<220>

<223> Modified Env/Tat/Rev

<400> 55

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20 25 30

Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45

Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60

Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80

Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95

Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp

100 105 110

Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Gly
115 120 125

Ala Gly Ser Cys Asn Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Val
130 135 140

Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala
145 150 155 160

Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Thr
165 170 175

Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser
180 185 190

Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile
195 200 205

Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr Ile Ile Val Gln Leu
210 215 220

Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
225 230 235 240

Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
245 250 255

Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Leu Gly Cys Thr Arg
260 265 270

Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile Gly Pro Gly Gln Thr
275 280 285

Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile Arg Gln Ala His Cys
290 295 300

Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gly Pro
305 310 315 320

Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln
325 330 335

Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile Arg Gln Arg Thr Pro
340 345 350

Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg Arg Ile Glu Asp Ile
355 360 365

Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr Asn Thr Arg Thr Ser
370 375 380

Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Thr
385 390 395 400

Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys Thr Arg Pro Asn Asn
405 410 415

Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly Arg Val Phe Tyr Thr
420 425 430

Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala His Cys Cys Thr Arg
435 440 445

Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe Ala Pro Gly Gln Ala
450 455 460

Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile Arg Gln Ala His Cys
465 470 475 480

Leu Gly Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Val Arg Ile
485 490 495

Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Asp Ile Ile Gly Asp Ile
500 505 510

Arg Gln Ala His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser
515 520 525

Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala Thr Gly Glu Ile Ile
530 535 540

Gly Asp Ile Arg Gln Ala His Cys Cys Thr Arg Pro Tyr Asn Asn Ile
545 550 555 560

Arg Gln Arg Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr Arg
565 570 575

Arg Ile Glu Asp Ile Arg Arg Ala His Cys Cys Thr Arg Pro Ser Thr
580 585 590

Asn Thr Arg Thr Ser Ile Arg Ile Gly Pro Gly Gln Val Phe Tyr Arg
595 600 605

Thr Gly Asp Ile Thr Gly Asp Ile Arg Lys Ala Tyr Cys Gly Ser Cys
610 615 620

Thr Arg Pro Asn Asn Asn Thr Arg Lys Arg Ile Ser Leu Gly Pro Gly
625 630 635 640

Arg Val Phe Tyr Thr Ala Gly Glu Ile Ile Gly Asp Ile Arg Lys Ala
645 650 655

His Cys Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Phe
660 665 670

Ala Pro Gly Gln Ala Leu Tyr Ala Thr Gly Glu Ile Ile Gly Asp Ile
675 680 685

Arg Gln Ala His Cys Leu Gly Asn Ile Ser Arg Ala Lys Trp Asn Asn
690 695 700

Thr Leu Lys Gln Ile Asp Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn
705 710 715 720

Lys Thr Ile Ile Phe Lys Gln Ser Ser Gly Gly Asp Pro Glu Ile Val
725 730 735

Thr His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr
740 745 750

Gln Leu Phe Asn Ser Thr Trp Phe Asn Ser Thr Trp Ser Thr Lys Gly
755 760 765

Ser Asn Asn Thr Glu Gly Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile
770 775 780

Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala
785 790 795 800

Pro Pro Ile Ser Gly Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu
805 810 815

Leu Leu Thr Arg Asp Gly Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe
820 825 830

Arg Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr
835 840 845

Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr Lys
850 855 860

Ala Lys Arg Arg Val Val Gln Thr Ser Ala Val Gly Ile Gly Ala Leu
865 870 875 880

Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly Cys Thr Ser
885 890 895

Met Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Asp Ile Val Gln
900 905 910

Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu
915 920 925

Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala
930 935 940

Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys
945 950 955 960

Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp
965 970 975

Ser Asn Lys Ser Leu Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu
980 985 990

Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile
995 1000 1005

Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu
1010 1015 1020

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr
1025 1030 1035

Asn Trp Leu Trp Tyr Ile Lys Leu Phe Ile Met Ile Val Gly Gly
1040 1045 1050

Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile Val Asn
1055 1060 1065

Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr His Leu
1070 1075 1080

Pro Ile Pro Arg Gly Pro Asp Arg Pro Glu Gly Ile Glu Glu Glu
1085 1090 1095

Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg Leu Val Asn Gly

1100 1105 1110

Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe
1115 1120 1125

Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr Arg Ile
1130 1135 1140

Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr Trp
1145 1150 1155

Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
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Val Asn Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu
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<211> 507

<212> DNA

<213> Human immunodeficiency virus type 1

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agacaaggaa ctgtatcctt taacttccct cagatcactc tttggcaacg acccctcgtc 240

acaataaaga taggggggca actaaaggaa gctctattag atacaggagc agatgataca 300

gtattagaag aaatgagttt gccaggaaga tggaaaccaa aaatgatagg gggaattgga 360

ggttttatca aagtaagaca gtatgatcag atactcatag aaatctgtgg acataaagct 420

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cagattggtt gcactttaaa ttttttaa 507

<210> 57

<211> 168

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 57

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20 25 30

Gln Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln Val Trp Gly
35 40 45

Arg Asp Asn Asn Ser Pro Ser Glu Ala Gly Ala Asp Arg Gln Gly Thr
50 55 60

Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val
65 70 75 80

Thr Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly
85 90 95

Ala Asp Asp Thr Val Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys
100 105 110

Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr
115 120 125

Asp Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val
130 135 140

Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr
145 150 155 160

Gln Ile Gly Cys Thr Leu Asn Phe
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<210> 58

<211> 1800

<212> DNA

<213> Artificial sequence

<220>

<223> Gag-PI

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ctagaacgat tcgcagttaa tcctggcctg ttagaaacat cagaaggctg tagacaaata 180

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caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480

gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc 540

ccacaagatt taaacaccat gctaaacaca gtgggggggac atcaagcagc catgcaaatg 600

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gctacactag aagaaatgat gacagcatgt cagggagtag gaggacccgg ccataaggca 1080

agagttttgg ctgaagcaat gagccaagta acaaatacag ctaccataat gatgcagaga 1140

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gaagctctat tagatacagg agcagatgat acagtattag aagaaatgag tttgccagga 1620

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cagatactca tagaaatctg tggacataaa gctataggta cagtattagt aggacctaca 1740

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<210> 59

<211> 599

<212> PRT

<213> Artificial sequence

<220>

<223> Gag-PI

<400> 59

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195 200 205

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Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
    210                 215                 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225                 230                 235                 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
                245                 250                 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
            260                 265                 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
        275                 280                 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
    290                 295                 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305                 310                 315                 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
                325                 330                 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
            340                 345                 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
        355                 360                 365

Gln Val Thr Asn Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
    370                 375                 380

Asn Gln Arg Lys Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
385                 390                 395                 400

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
                405                 410                 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
            420                 425                 430

Phe Phe Arg Glu Asp Leu Ala Phe Leu Gln Gly Lys Ala Arg Glu Phe
        435                 440                 445

Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Ile Ser Ser Glu Gln
    450                 455                 460
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Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln Val Trp Gly Arg
465 470 475 480

Asp Asn Asn Ser Pro Ser Glu Ala Gly Ala Asp Arg Gln Gly Thr Val
485 490 495

Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr
500 505 510

Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala
515 520 525

Asp Asp Thr Val Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro
530 535 540

Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp
545 550 555 560

Gln Ile Leu Ile Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu
565 570 575

Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln
580 585 590

Ile Gly Cys Thr Leu Asn Phe
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<210> 60

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 60
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<210> 61

<211> 42

<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

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<210> 62

<211> 41

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<400> 62
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<210> 63

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<210> 65

<211> 36

<212> DNA

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<400> 65
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<210> 66

<211> 36

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<400> 66
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<210> 67

<211> 47

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<210> 68

<211> 47

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<210> 71

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<212> DNA

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<400> 71
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<210> 72

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<212> DNA

<213> Artificial sequence

<220>

<223> MMLV SD site

<400> 72
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<210> 73

<211> 9

<212> DNA

<213> Artificial sequence

<220>

<223> MMLV SA site

<400> 73
ctgctgcag 9

<210> 74

<211> 90

<212> DNA

<213> Artificial sequence

<220>

<223> DNA encoding gp120 signal peptide

<400> 74
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ctccttggga tgttgatgat ctgtagtgct 90

<210> 75

<211> 129

<212> DNA

<213> Artificial sequence

<220>

<223> DNA encoding gp41 transmembrane domain

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gtagtgaata gagttaggca gggatattca ccattatcgt ttcagaccca cctcccaatc 120

ccgagggga 129